



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 97723

TO: Lisa V Cook

Location: cm-1/7b17/7e12

Art Unit : 1641

Thursday, July 10, 2003

Case Serial Number: 851058

From : Susan Hanley

Location: Biotech-Chem Library

CM1 6B05

Phone: 305-4053

susan.hanley@uspto.gov

Search Notes

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STANISLAWSKI

Scientific and Technical Information Center

Requester's Full Name: Lisa V Cook Examiner #: 77134 Date: 4/30/03
 Art/Unit: 1641 Phone Number: 305-208-0808 Serial Number: 09/851,058
 Mail Box and Bldg/Rm Location: CMI 77134 Results Format Preferred (circle): PAPER DISK E-MAIL

Office: CMI 77134

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures; keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations/authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Process for analyzing protein samples

Inventors (please provide full names): Kenneth C. Porker, Timothy K. Nadler, George J. Yella, Rudolf Abbersold, Marcus Smolka

Earliest Priority Filing Date: 5/8/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Sequence Search, including interference Search.

Seq. ID NO: 1
 Seq. ID NO: 2 > all three EST's
 Seq. ID NO: 3

labeled peptides
 also see attached claims and bib sheet

RECEIVED
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MICHIGAN
(STIC)

10
 seq 1 2 3
 1 2 3

NA

Thanks
Lisa C.

STAFF USE ONLY

Searcher: Hawley

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: 7/8

Date Completed: 7/10

Searcher Prep & Review Time: 3

Type of Search

NA Sequence (#) _____

AA Sequence (#) 3 _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems ab5502

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GenCore version 5.1.6
copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: July 9, 2003, 11:55:35 ; (Search time 44 Seconds
(without alignments))
30.284 Million cell updates/sec

Title: US-09-851-058-1
Perfect score: 54

Sequence: 1 QLPCPAELLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesed_101002:*

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2: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1981.DAT: *
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6: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1985.DAT: *
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8: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1987.DAT: *
9: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1988.DAT: *
10: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1989.DAT: *
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12: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1991.DAT: *
13: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1992.DAT: *
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20: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA1999.DAT: *
21: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA2001.DAT: *
22: /SIDS2/gcdatal/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	54	100.0	476 22	AAU29351 Novel mar regulated proteinbacterium
2	45	83.3	79 22	AAU59483 Human immune/haema
3	41	75.9	50 22	AAW8485 Human pancreatic cancer assoc
4	41	75.9	78 21	AAH54100 Human MLN 64. Hom C. trachomatis OMC C. trachomatis OMC Chlamydia trachoma
5	41	75.9	180 21	AAH43728 Human MLN 64. Hom C. trachomatis OMC C. trachomatis OMC Chlamydia trachoma
6	41	75.9	445 18	AAW25768 WPI: 2001-602769/68. NP-PSDR: AA46251.
7	39	72.2	20 21	AAB13666 Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound
8	39	72.2	20 21	ABR13667 PT
9	39	72.2	20 22	AAG8334 PT
10	39	72.2	20 22	AAG83235 PT

ALIGNMENTS

11	39	72.2	20	23	ABB94205 Chlamydia peptide			
12	39	72.2	20	23	ABB94206 Chlamydia peptide			
13	39	72.2	51	20	AAV17695 Human 5', EST secre			
14	39	72.2	132	22	ARE03341 Human gene 17 enco			
15	39	72.2	132	23	ABG6431 Human albumin fusi			
16	39	72.2	143	22	AAE01308 Human gene 17 enco			
17	39	72.2	143	23	ABG6434 Human albumin fusi			
18	39	72.2	234	19	AAM33973 Pseudomonas fluoresc			
19	39	72.2	252	15	ABB04126 Chlamydia trachoma			
20	39	72.2	553	20	ABY37788 Chlamydia trachoma			
21	39	72.2	553	23	ABB94288 Propionibacterium			
22	39	72.2	554	23	AAE02293 Peptide #7043 enco			
23	38	70.4	41	22	AAM62233 Human bone marrow			
24	38	70.4	41	22	AAM72118 Human brain express			
25	38	70.4	41	22	AAM72858 Zea mays protein f			
26	38	70.4	41	22	AAM31089 Pseudomonas aerugi			
27	38	70.4	41	23	ABG46688 Drosophila melanog			
28	37	68.5	405	22	ABB67386 Propionibacterium			
29	37	68.5	420	23	ABR0836 Corynebacterium gl			
30	37	68.5	420	22	AAU28066 Novel human secret			
31	37	68.5	1025	22	AAU31447 Novel human secret			
32	37	68.5	1025	22	AAU31447 Novel human diagno			
33	37	68.5	1376	22	ABG24780 Human peptide enco			
34	37	68.5	76	22	AAO04418 Human secreted pro			
35	37	68.5	41	36	66.7	19	AAW7752 Human immunohaema	
36	37	68.5	42	36	66.7	178	AAW84911 Propionibacterium	
37	37	68.5	43	36	66.7	262	AAU41650 Drosophila melanog	
38	37	68.5	44	36	66.7	890	AAU6723 Novel human diagno	
39	37	68.5	45	35	64.8	37	22	ABG11041 Chlamydia trachoma

PS Disclosure; page 302-303; 526pp; English.

XX

CC The invention relates to a method of identifying compounds that modulate CC a newly identified marker regulated (NMR) polypeptide activity. The method CC comprises contacting an NMR polypeptide with a test compound under CC interaction conditions, determining the ability of the compound to CC modulate the activity or expression of the polypeptide, and selecting the CC modulators. NMR nucleic acids and polypeptides are used in the treatment CC of microbial infections, and in screening for modulators or NMR CC expression and activity. These modulators can be used to reduce the CC infectivity of a microbe on a surface, and the virulence of a microbe in CC a subject suffering from an infection. AU29326-AU29379 represent CC Escherichia coli NMR amino acid sequences of the invention.

XX

SQ Sequence 476 AA;

Query Match	Best Local Similarity	Score	DB	Length
Matches 10;	Conservative	54	22;	476;
Oy 1	LQPCPAELLR 10			
Db 415	QLPCPAELLR 424			

RESULT 2

Query Match	Best Local Similarity	Score	DB	Length
Matches 10;	Conservative	54	22;	476;
Oy 1	LQPCPAELLR 10			
Db 415	QLPCPAELLR 424			

AU59483

ID AAU59483 standard; Protein: 79 AA.

XX

AC AAU59413;

XX

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #20379.

XX

KW SAPHO syndrome; Synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

PN WO200181581-A2.

PD 01-NOV-2001.

XX

PP 20-APR-2001; 2001WO-US12865.

XX

PR 21-APR-2000; 2000US-193047P.

PR 07-JUL-2000; 2000US-208841P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Skeky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX

DR WPI; 2001-616774/71.

DR XX

PT Propionibacterium acnes polypeptides and nucleic acids useful for PT vaccinating against and diagnosing infections, especially useful for PT treating acne vulgaris - Example 1; SEQ ID NO 20678; 1069pp; English.

PS Sequences AU39105-Au68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis. CC Acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient: comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC

SQ Sequence 79 AA;

Query Match	Best Local Similarity	Score	DB	Length
Matches 8;	Conservative	45	22;	79;
Oy 2	LPCPAELLR 10			
Db 54	LPCPAELLR 62			

RESULT 3

Query Match	Best Local Similarity	Score	DB	Length
Matches 8;	Conservative	45	22;	79;
Oy 2	LPCPAELLR 10			
Db 54	LPCPAELLR 62			

AAM88485

ID AAM88485 standard; Protein: 50 AA.

XX

AC AAM8845;

XX

DT 07-NOV-2001 (first entry).

DE Human immune/haematopoietic antigen SEQ ID NO:16078.

XX

KW Human; immune; haemopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.

XX

OS Homo sapiens.

XX

PN WO200157192-A2.

PD 09-AUG-2001.

XX

PP 17-JAN-2001; 2001WO-US01354.

XX

PR 31-JAN-2000; 2000US-0179055.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216830.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0217496.

PR 26-JUL-2000; 2000US-0220933.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225314.

PR 14-AUG-2000; 2000US-022566.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-023270.

PR 14-AUG-2000; 2000US-022447.

PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-022219.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0228947.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 03-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0231267.
 PR 06-SEP-2000; 2000US-0230438.
 PR 06-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233059.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234997.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 29-SEP-2000; 2000US-0236371.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240650.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241803.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 01-NOV-2000; 2000US-0244644.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249300.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0249300.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PT Rosen CA, Barash SC, Ruben SM;
 XX DR N-PSDB; AAK61266.
 PS Claim 11; SEQ ID NO 16078; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAW82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK7694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 CC
 SO Sequence 50 AA;

Query	Match	Score	Length
Best Local Similarity	100.0%	41	DB 22;
Matches	7;	Seq	Length 50;
Conservative	0;	Pred. No.	10;
Mismatches	0;	Indels	0;
		Gaps	0;
		Caps	0;

QY	1 QLPCPAE 7	Best Local Similarity 87.5%	Pred. No. 16	Matches 7; Conservative	1; Mismatches 0;	Indels 0;	Gaps 0;
Db	1						
RESULT 4							
ID AAB54300	XX						
ID AAB54300 standard; Protein; 78 AA.	XX						
AC AAB54300;	XX						
DT 09-MAR-2001 (first entry)	XX						
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:752.	XX						
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytotoxic; neuroprotective; nootropic; immunomodulatory; cardiotonic; relaxant; contraceptive; gynaecological; linkage analysis; tissue identification; tissue typing; forensic; pulmonary; cardiovascular; renal; proliferative.	XX						
KW Homo sapiens.	XX						
XX WO2000055320-A1.	XX						
XX PR 21-SEP-2000.	XX						
XX P1 08-MAR-2000; 2000NO-US05989.	XX						
XX PR 12-MAR-1999; 99US-0124270.	XX						
XX DR N-PSDB; AAC9065.	XX						
XX P1 Rosen CA, Ruben SM;	XX						
XX PR WPI; 2000-579444-54.	XX						
XX DR (HUMA-) HUMAN GENOME SCI INC.	XX						
XX P1 New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition -	XX						
XX PS Claim 11; Page 1195-1196; 137pp; English.	XX						
CC AAC9873 to AAC9231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB4008 to AAB4466, the human pancreatic cancer antigens have cytotoxic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiotonic and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or sequences used in the exemplification of the present invention.	XX						
CC Sequence 78 AA;	XX						
XX Query Match	XX						
XX 75.9%; Score 41; DB 21; Length 78;	XX						
QY 2 LPCHAEELL 9	Best Local Similarity 87.5%	Pred. No. 16	Matches 7; Conservative	1; Mismatches 0;	Indels 0;	Gaps 0;	
Db 54 LPCFAELV 61	1						
RESULT 5							
ID AAB43728	XX						
ID AAB43728 standard; Protein; 180 AA.	XX						
AC AAB43728;	XX						
DT 08-FEB-2001 (first entry)	XX						
DE Human cancer associated protein sequence SEQ ID NO:1173.	XX						
KW Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; anti rheumatic; antiarthritic; antiviral; dermatological; neuroprotective; thrombolytic; coagulant; vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haemopoietic; cellular disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; neurological disease; drug screening.	XX						
KW Homo sapiens.	XX						
XX WO2000055350-A1.	XX						
XX PR 21-SEP-2000.	XX						
XX P1 08-MAR-2000; 2000NO-US05982.	XX						
XX PR 12-MAR-1999; 99US-0124270.	XX						
XX PA (HUMA-) HUMAN GENOME SCI INC.	XX						
XX PI Rosen CA, Ruben SM;	XX						
XX DR WPI; 2000-587533-55.	XX						
XX DR N-PSDB; AAC77937.	XX						
XX PT Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.	XX						
XX PS Claim 11; Page 1794-1795; 235pp; English.	XX						
CC AAC77607 to AAC78448 encode the human cancer associated proteins given in AAC93398 to AAC41239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytotoxic; proliferative; vulnerary; immunomodulator; antidiabetic; antiinflammatory; antihistamic; anti rheumatic; antiarthritic; dermatological; neuroprotective; cardiotonic; thrombolytic; coagulant; nootropic; vasotrophic; antipsoriatic; and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haemopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulating haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC778449 to AAC78457 and AAC41240 represent sequences used in the exemplification of the present invention.	CC						

Sequence	180 AA;	Score	41;	DB	21;	Length	180;
Query Match	75.9%	Score	41;	DB	21;	Length	180;
Best Local Similarity	87.5%	Pred.	No.	34;			
Matches	7;	Conservative	1;	Mismatches	0;	Indels	0;
Qy	2	LPCPAELL 9	:				
Db	24	LPCPAELV 31	:				
RESULT 6							
AAN25768							
ID AAN25768 standard; Protein; 445 AA.							
XX							
AC AAN25768;							
XX							
DT 05-DEC-1997 (first entry)							
XX							
DE Human MLN 64.							
XX							
KW Human; CART1; Lasp-1; MLN 64; MLN 51; hds3; mds2; breast carcinoma cell; CYS-rich region; RING finger domain; CART motif; TRAF domain; LIM domain; TNF-related cytokine signal transduction; breast cancer; SH3; Src homology region 3.							
XX							
OS Homo sapiens.							
XX							
FH Key	Location/Qualifiers						
FT Domain	1..72						
FT Domains	/label= Potential_Transmembrane_domain						
FT Domains	94..108						
FT Domains	/label= Potential_Transmembrane_domain						
XX							
PN W09706256-A2.							
XX							
PR 20-FEB-1997.							
XX							
PR 31-JUL-1996; 96WO-US12500.							
XX							
PR 09-AUG-1995; 95US-0002183.							
XX							
PA (BRIM) BRISTOL-MYERS SQUIBB CO.							
PA (CNRS) CENT NAT RECH SCI.							
PA (INRA) INST NAT SANTE & RECH MEDICALE.							
PA (UVEA) UNIV PASTEUR LOUIS.							
XX							
PT Basset P, Byrne J, Rio M, Tomasetto C;							
XX							
DR WPI; 1997-154263/14.							
DR N-PSSB; AATB6171.							
XX							
PT Genes amplified and over-expressed in breast carcinoma - located on chromosome 17 q11-q21.3 or 6 q22-q23, useful in breast cancer							
PT prognosis and as leukemia markers							
XX							
PS Claim 11; Fig 16; 197pp; English.							
XX							
CC This sequence is human MLN 64 encoded by DNA deposited as ATCC 97609.							
CC The MLN 64 gene has been mapped to the q12-q21 region of the long arm							
CC of chromosome 17 with the maximum in the q21.1. This region already							
CC contains two genes known to be involved in breast cancer. The MLN 64							
CC gene contains 15 exons. There are 7 distinct MLN 64 cDNAs resulting							
CC from nucleotide substitutions, deletions and/or insertions. These							
CC modifications mainly occur at intron/exon boundaries, suggesting that							
CC the MLN 64 variants result from defective splicing processes. Two							
CC variants lead to amino acid variants and 5 variants encode N- or							
CC C-truncated MLN 64 proteins. Also, 3 of these lead to chimeric proteins							
CC containing additional nonsense protein sequences of 15, 20 and 126							
CC residues. The full length MLN 64 protein has two potential							
CC leucine-rich repeat structures. The MLN 64 gene and protein are							
CC useful as prognostic markers for breast cancer.							
XX							
SQ Sequence 445 AA;							
Query Match	75.9%	Score	41;	DB	18;	Length	445;
Best Local Similarity	87.5%	Pred.	No.	77;			
Matches	7;	Conservative	1;	Mismatches	0;	Indels	0;
Qy	2	LPCPAELL 9	:				
Db	289	LPCPAELV 296	:				
RESULT 7							
AAB13666							
ID AAB13666 standard; Peptide; 20 AA.							
XX							
AC AAB13666;							
XX							
DT 02-FEB-2001 (first entry)							
XX							
DE C. trachomatis ORCB peptide 133-152.							
XX							
KW Chlamydial infection; sexually transmitted disease; infertility;							
KW trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.							
XX							
OS Chlamydia trachomatis.							
XX							
PN W020034483-A2.							
XX							
PD 15-JUN-2000.							
XX							
PP 08-DEC-1999; 99WO-US29012.							
XX							
PR 08-DEC-1998; 98US-0208277.							
PR 08-APR-1999; 99US-0288594.							
PR 01-OCT-1999; 99US-0410568.							
PR 22-OCT-1999; 99US-0426571.							
XX							
PA (CORI-) CORIXA CORP.							
XX							
PI Probst P, Bhatia A, Skeiky YAN, Fling SP, Jen S, Stromberg EJ;							
DR WPI; 2000-431303/37.							
XX							
PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection							
PT comprises immunogenic portion of Chlamydia antigen, which comprises							
PT amino acid sequence encoded by Polynucleotide sequence							
XX							
PS Disclosure; Page 231; 256pp; English.							
XX							
CC The present invention relates to new nucleic acid sequences and the							
CC proteins encoded by the nucleic acid sequences. The encoded proteins							
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded							
CC proteins are useful for the serodiagnosis and treatment of Chlamydia							
CC infection. Chlamiae are intracellular bacterial pathogens that are							
CC responsible for a wide variety of human infections. C. trachomatis							
CC infection is one of the most common sexually transmitted diseases and can							
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction							
CC and infertility. Trachoma due to ocular infection with C. trachomatis is							
CC the leading cause of preventable blindness worldwide. C. pneumoniae is a							
CC major cause of acute respiratory tract infections in humans and is also							
CC thought to play a role in the pathogenesis of atherosclerosis and the							
CC coronary heart disease. The present sequence is a protein isolated in the							
CC present invention.							
XX							
SQ Sequence 20 AA;							
Query Match	72.2%	Score	39;	DB	21;	Length	20;
Best Local Similarity	70.0%	Pred.	No.	9.6;			
Matches	7;	Conservative	1;	Mismatches	2;	Indels	0;
Gaps	0;						

XX
PN WO200140474-A2.
XX
PT Novel compositions comprising Chlamydia Cap1 protein and its use in the
XX treatment of Chlamydia infection -
XX
PF Disclosure; Page 266; 537pp; English.

XX
PR 03-DEC-1999; 990US-0454684.
XX
PR 19-APR-2000; 2000US-0556877.
XX
PR 20-JUN-2000; 2000US-0558419.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
XX
WPI: 2001-374831/39.
XX
PT Chlamydia polypeptides and fusion proteins useful for preventing pelvic
XX inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease -
XX
PS Claim 66; Page 237; 295pp; English.
XX
CC The present peptide is provided in a specification relating to
compounds and methods for the treatment and diagnosis of chlamydial
infection. The compounds provided include polypeptides and fusion
proteins comprising immunogenic portions of Chlamydia antigens
and DNA sequences encoding such polypeptides. They are useful for
vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX
SQ Sequence 20 AA:
Query Match 72.2%; Score 39; DB 22; Length 20;
Best Local Similarity 70.0%; Pred. No. 9.6; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QLPCEFAELLR 10
||| || :|
3 QLPCEAEFVR 12
Db
XX
RESULT 11
ABB94205
ID ABB94205 standard; Peptide; 20 AA.
XX
AC ABB94205;
XX
DT 05-JUN-2002 (first entry)
XX
DE Chlamydia peptide sequence SEQ ID NO:242.
XX
KW Chlamydial infection; Chlamydia; vaccine; detection; diagnosis;
KW antigen; antibacterial; immunostimulant; immune response;
KW Chlamydia-specific T-cell response.
XX
OS Synthetic.
XX
PN WO200208267-A2.
XX
PD 31-JAN-2002.
XX
PE 20-JUL-2001; 2001WO-US23121.
XX
PR 20-JUL-2000; 2000US-0620412.
PR 23-APR-2001; 2001US-0841132.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fling SP, Skeiky YAW, Probst P, Bhatia A;
XX
PR WPI; 2002-179901/23.
XX
PT Novel compositions comprising Chlamydia Cap1 protein and its use in the
XX treatment of Chlamydia infection -
XX
PS Disclosure; Page 266; 537pp; English.
XX
The present invention describes compositions comprising a Chlamydia Cap1
CC protein and methods for the diagnosis and therapy of Chlamydia infection.
CC Chlamydia DNA and protein sequences from the present invention can have
CC antibacterial and immunostimulant activities, and can be used in
CC vaccines. Compounds from the present invention can be used for eliciting
an immune response, specifically stimulating a Chlamydia specific T-cell
response or inhibiting the development of a Chlamydia infection in an
animal. Methods from the present invention can be used: for detecting the
presence of Chlamydia in a patient; to stimulate and/or expand T cells
specific for a Chlamydia protein; and for treatment of a Chlamydia
infection. ABB9294 to ABB92709 and ABB94374 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 20 AA:
Query Match 72.2%; Score 39; DB 23; Length 20;
Best Local Similarity 70.0%; Pred. No. 9.6; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QLPCEFAELLR 10
||| || :|
Db 7 QLPCEAEFVR 16
XX
RESULT 12
ABB94206
ID ABB94206 standard; Peptide; 20 AA.
XX
AC ABB94206;
XX
DE Chlamydia peptide sequence SEQ ID NO:243.
XX
KW Chlamydial infection; Chlamydia; vaccine; detection; diagnosis;
KW antigen; antibacterial; immunostimulant; immune response;
KW Chlamydia-specific T-cell response.
XX
OS Synthetic.
XX
PN WO200208267-A2.
XX
PR 31-JAN-2002.
XX
PE 20-JUL-2001; 2001WO-US23121.
XX
PR 20-JUL-2000; 2000US-0620412.
PR 23-APR-2001; 2001US-0841132.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fling SP, Skeiky YAW, Probst P, Bhatia A;
XX
PR WPI; 2002-179901/23.
XX
PT Novel compositions comprising Chlamydia Cap1 protein and its use in the
XX treatment of Chlamydia infection -
XX
PS Disclosure; Page 266; 537pp; English.
XX
The present invention describes compositions comprising a Chlamydia Cap1
CC protein and methods for the diagnosis and therapy of Chlamydia infection.
CC Chlamydia DNA and protein sequences from the present invention can have
CC antibacterial and immunostimulant activities, and can be used in
CC vaccines. Compounds from the present invention can be used for eliciting

CC protein genes, and AAE03392-AAE03346 represent the proteins they encode.
 CC AAE03347-AAE03375 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing, XX
 CC treating or ameliorating medical conditions, e.g., by protein or gene XX
 CC therapy. Pathological conditions can be diagnosed by determining the XX
 CC amount of the new protein in a sample or by determining the presence of XX
 CC mutations in the new genes. Specific uses are described for each of the XX
 CC 19 genes, based on the tissues in which they are most highly expressed, XX
 CC and include developing products for the diagnosis or treatment of PS
 CC proliferative disorders, cancer, tumours, foetal and developmental PS
 CC abnormalities, haematopoietic disorders, diseases of the immune system, PS
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, PS
 CC allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and CC in diagnostic immunoassays e.g., radioluminoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human CC secreted protein of the invention.

XX sequence 132 AA;

SO Sequence 132 AA;

Query Match 72.2%; Score 39; DB 22; Length 132;
 Best Local Similarity 77.8%; Pred. No. 54;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLPCPABEL 9
 Db 91 ELPCPABHL 99

RESULT 15

ID ABG64431
 XX ABG64431 standard; Protein; 132 AA.
 AC ABG64431;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human albumin fusion protein #1106.
 XX
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antinefertile; antiinflammatory; antilulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO20017137-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US11988.
 XX
 PR 12-APR-2000; 2000US-229350P.
 PR 25-APR-2000; 2000US-199384P.
 PR 21-DEC-2000; 2000US-256931P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX Sequence 132 AA;

Query Match 72.2%; Score 39; DB 23; Length 132;
 Best Local Similarity 77.8%; Pred. No. 54;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLPCPABEL 9
 Db 91 ELPCPABHL 99

Search completed: July 9, 2003, 12:00:05
 Job time : 46 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:58:36 ; search time 22.5 Seconds

(without alignments) 13.077 Million cell updates/sec

Title: US-09-851-058-1

Perfect score: 54 QLPCPAELLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

US-08-691-814B-6

; Sequence 6, Application US/08691814B

GENERAL INFORMATION:

APPLICANT: RIC, Marie-Christine

APPLICANT: Basset, Paul

APPLICANT: Byrne, Jennifer

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful

TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave, NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/691,814B

FILING DATE: 31-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,183

FILING DATE: 09-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1383.0090001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

; US-08-691-814B-6

Query Match Score 41; DB 2; Length 445;

Best Local Similarity 87.5%; Pred. No. 18;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Appli

Sequence 1, Appli

Sequence 2, Appli

Sequence 8, Appli

Sequence 2, Appli

Sequence 1, Appli

Sequence 56, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 1, Appli

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Run on: July 9, 2003, 11:58:36 ; search time 22.5 Seconds

(without alignments) 13.077 Million cell updates/sec

Title: US-09-851-058-1

Perfect score: 54 QLPCPAELLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY 2 LQPCPAELL 9
 |||||||:
 Db 289 LQCPAELV 295

RESULT 2 ; Sequence 242, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C7
 ; CURRENT APPLICATION NUMBER: US/09/556,877
 ; CURRENT FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
 ; SEQ ID NO: 242
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-556-877-242

Query Match
 Best Local Similarity 72.2%; Score 39; DB 4; Length 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLPCPAELLR 10
 Dv 7 QLPCAEFVR 16

RESULT 3 ; Sequence 243, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556,877
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
 SEQ ID NO 243
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-556-877-243

Query Match
 Best Local Similarity 70.0%; Score 39; DB 4; Length 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLPCPAELL 10
 Dv 7 QLPCAEFVR 16

RESULT 4 ; Sequence 242, Application US/09620412C
 ; Patent No. 6448234
 ; GENERAL INFORMATION:
 ; APPLICANT: Steven P. Fling
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C7
 ; CURRENT APPLICATION NUMBER: US/09/620,412C
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
 ; SEQ ID NO: 242
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-620-412C-242

Query Match
 Best Local Similarity 72.2%; Score 39; DB 4; Length 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLPCPAELL 10
 Dv 7 QLPCAEFVR 16

RESULT 5 ; Sequence 243, Application US/09620412C
 ; Patent No. 6448234
 ; GENERAL INFORMATION:
 ; APPLICANT: Steven P. Fling
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C7
 ; CURRENT APPLICATION NUMBER: US/09/620,412C
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
 ; SEQ ID NO: 243
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-620-412C-243

Query Match
 Best Local Similarity 72.2%; Score 39; DB 4; Length 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLPCPAELL 10
 Dv 7 QLPCAEFVR 12

RESULT 6 ; Sequence 8, Application US/08411777
 ; Patent No. 5792641
 ; GENERAL INFORMATION:
 ; APPLICANT: Schulein, Martin
 ; APPLICANT: Fredholm, Henrik
 ; APPLICANT: Hjorth, Carsten
 ; APPLICANT: Rasmussen, Grethe
 ; APPLICANT: Nielsen, Egon
 ; APPLICANT: Rosholm, Peter
 ; TITLE OF INVENTION: Cellulase Variants
 ; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 57926410 NO. 5792641th America
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,777
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gregg, Valeta A.
 REGISTRATION NUMBER: 35,127
 REFERENCE/DOCKET NUMBER: 3913.504-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-868-9655
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: NO. 5792641e
 US-08-411-777-8
 Db 226 EVPCPAEL 233

RESULT 7
 US-09-057-088-B
 ; Sequence 8, Application US/09/057/088
 ; Parent No. 6114296
 GENERAL INFORMATION:
 APPLICANT: Schuhlein, Martin
 APPLICANT: Fredholm, Henrik
 APPLICANT: Hjorth, Carsten
 APPLICANT: Rasmussen, Grethe
 APPLICANT: Nielsen, Egon
 APPLICANT: Rosholm, Peter
 TITLE OF INVENTION: Cellulase Variants
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 61142960 NO. 6114296th America
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/057,088
 FILING DATE:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/411,777
 FILING DATE: 05-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Gregg, Valeta A.
 REGISTRATION NUMBER: 35,127
 REFERENCE/DOCKET NUMBER: 3913.504-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-868-9655
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: NO. 6114296e
 US-09-057-088-B
 Query Match 72.2%; Score 39; DB 1; Length 252;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 0;
 Qy 1 OLPCPAEL 8
 Db 226 EVPCPAEL 233

RESULT 8
 US-09-149-476-341
 ; Sequence 341, Application US/09/149/476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 186 Human Secreted Proteins
 FILE REFERENCE: PZ002P1
 CURRENT APPLICATION NUMBER: US/09/149,476
 CURRENT FILING DATE: 1998-09-08
 EARLIER APPLICATION NUMBER: PCN/US98/04493
 EARLIER FILING DATE: 1998-03-05
 EARLIER APPLICATION NUMBER: 60-040,162
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60-040,333
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60-038,621
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60-040,336
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60-040,163
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60-047,600
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,615
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,597
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,502
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,633
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,583
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,617
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60-047,618
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,503

FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERRAL/DOCKET NUMBER: 3313.504-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-868-9655
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6114296e
US-09-057-088-10

Query Match 64.8%; Score 35; DB 3; Length 284;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 1 OLPCPAELL 9
Db 186 QVQCPAELV 194

RESULT 12
US-09-230-225B-6
Sequence 6, Application US/09230225B
Patent No. 6,03362
GENERAL INFORMATION:
APPLICANT: Meiji Seika Kaisha, Ltd.
TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides by Microorganism
FILE REFERENCE: VA990054
CURRENT APPLICATION NUMBER: US/09/230,225B
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 285
TYPE: PRT
ORGANISM: Humicola insolens
US-09-230-225B-6

Query Match 64.8%; Score 35; DB 4; Length 285;
Best Local Similarity 66.7%; Pred. No. 1.1e+02; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 OLPCPAELL 9
Db 187 QVQCPAELV 195

RESULT 13
US-09-054-733-3
Sequence 3, Application US/09254733
Patent No. 6,277596
GENERAL INFORMATION:
APPLICANT: WATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: AOKI, KAORU
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING FROM INVENTION: IN TRICHOLOMMA VIRIDE AND SYSTEM FOR MASS-PRODUCING PROTEINS OR PEPTIDES THEREWITH
FILE REFERENCE: 99-0266/LC(WMC)-00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52

RESULT 14
US-09-189-060B-72
Sequence 72, Application US/09189060B
Patent No. 6,270968
GENERAL INFORMATION:
APPLICANT: Dalboe, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Kauppinen, Markus
APPLICANT: Borg, Diderichsen
TITLE OF INVENTION: Method Of Providing No. 6,270968el DNA Sequences
FILE REFERENCE: 4772-204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIORITY APPLICATION NUMBER: PCT/DK97/00216
PRIORITY FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 304
TYPE: PRT
ORGANISM: Hybrid
US-09-189-060B-72

RESULT 15
US-08-090-013-2
Sequence 2, Application US/08090013
Patent No. 5,433750
GENERAL INFORMATION:
APPLICANT: CONVENTS, ANDRE C
APPLICANT: BUSCH, ALFRED
APPLICANT: BAICK, ANDRE C
TITLE OF INVENTION: DETERGENT COMPOSITION WITH HIGH ACTIVITY
TITLE OF INVENTION: CELLULOSE AND SOFTENING CLAYS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER & GAMBLE COMPANY
STREET: 5299 SPRING GROVE AVENUE
CITY: CINCINNATI
STATE: OHIO
COUNTRY: USA
ZIP: 45217
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,013

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91202880.0
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATEL, KEN K.
REGISTRATION NUMBER: 33,988
REFERENCE/DOCKET NUMBER: CM393
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-6337
TELEFAX: 513-627-4854
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-090-013-2

Query Match 64.8%; Score 35; DB 1; Length 305;
Best Local Similarity 66.7%; Pred. No. 1.2e+02; Mismatches 2;
Matches 6; Conservative 2; Indels 1; Gaps 0;
Qy 1 QLPCPARELL 9
|: |||||:
Db 207 QVOCPARELV 215

Search completed: July 9, 2003, 12:03:34
Job time : 23.5 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:02:11 ; Search time 40.5 seconds
(without alignments) 28.746 Million cell updates/sec

Title: US-09-851-058-1

Perfect score: 54 QLPCPAELLR 10

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaas/PCT_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pubpaas/US06_NEW_PUB.pep: *
4: /cgn2_6/ptodata/1/pubpaas/US05_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaas/US04_PUBCOMB.pep: *
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10: /cgn2_6/ptodata/1/pubpaas/US10_NEW_PUB.pep: *
11: /cgn2_6/ptodata/1/pubpaas/US10_PUBCOMB.pep: *
12: /cgn2_6/ptodata/1/pubpaas/US10_PUBCOMB.pep: *
13: /cgn2_6/ptodata/1/pubpaas/US60_NEW_PUB.pep: *
14: /cgn2_6/ptodata/1/pubpaas/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	41	75.9	78	10 US-09-925-297-752 Sequence 752, App Sequence 1173, App
2	41	75.9	180	10 US-09-925-301-1173 Sequence 441, App
3	41	75.9	445	9 US-10-177-293-296 Sequence 296, App
4	39	72.2	20	10 US-09-841-132-242 Sequence 242, App
5	39	72.2	20	10 US-09-841-132-243 Sequence 243, App
6	39	72.2	235	9 US-09-241-328-10 Sequence 10, App
7	39	72.2	553	10 US-09-841-132-441 Sequence 441, App
8	38	70.4	41	10 US-09-764-761-3975 Sequence 4395, A
9	37	68.5	87	10 US-09-864-761-46356 Sequence 46356, A
10	37	68.5	284	10 US-09-815-242-11778 Sequence 11778, A
11	37	68.5	420	10 US-09-946-142-420 Sequence 2, App
12	36	66.7	106	9 US-09-805-391-341 Sequence 341, App
13	35	64.8	100	9 US-09-754-891-2875 Sequence 2875, App
14	35	64.8	118	9 US-09-764-860-1062 Sequence 1062, App
15	35	64.8	118	9 US-09-955-999-71 Sequence 1173, Application US/09925301
16	35	64.8	123	9 US-09-744-860-630 Sequence 630, App
17	35	64.8	128	9 US-09-764-860-1074 Sequence 1074, App
18	35	64.8	128	9 US-09-955-999-102 Sequence 102, App
19	35	64.8	143	9 US-09-764-868-1075 Sequence 1075, App

ALIGNMENTS

RESULT 1
US-09-925-297-752
Sequence 752, Application US/09925297
; Patent No. US20020052308A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIORITY NUMBER: PCT/US00/03989
; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 752
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (72)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-297-752

Query Match Score 75.9%; Score 41; DB 10; length 78;
Best Local Similarity 87.5%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQLCPAELL 9
Db 54 LQLCPAELV 61

RESULT 2
US-09-925-301-1173
; Sequence 1173, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAJ06
; CURRENT APPLICATION NUMBER: US/09/925, 301
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05082
; PRIORITY APPLICATION NUMBER: 60/124, 270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1173
; LENGTH: 180
; TYPE: PRT

ORGANISM: Homo sapiens
FEATURE: NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; IS-09-925-301-1173

Query Match Best Local Similarity 75.9%; score 41; DB 10; Length 180;
Best Local Similarity 87.5%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPCPAELL 9
Db 289 LPCPAELV 296

RESULT 3
IS-10-177-293-296
Sequence 296 Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Giatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Ganavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Roushen
APPLICANT: Xu, Yongqiao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Saini, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177-293
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/299, 887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301, 572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306, 501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325, 002
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/362, 585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx, xxx
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 296
LENGTH: 445
TYPE: PRT

RESULT 4
US-09-841-132-242
Sequence 242 Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhattacharya, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TIME OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT APPLICATION NUMBER: US/09/841, 132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO: 242
LENGTH: 20

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
; IS-09-841-132-242

Query Match Best Local Similarity 70.0%; score 39; DB 10; Length 20;
Best Local Similarity 70.0%; Pred. No. 3.1; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OLPCPAELLR 10
Db 7 QLPCEAEFVR 16

RESULT 5
US-09-841-132-243
Sequence 243 Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhattacharya, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT APPLICATION NUMBER: US/09/841, 132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO: 243
LENGTH: 20

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
; IS-09-841-132-243

Query Match Best Local Similarity 72.2%; score 39; DB 10; Length 20;
Best Local Similarity 70.0%; Pred. No. 3.1; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OLPCPAELL 10

Db 3 OLPCEAECVR 12

RESULT 6

; Sequence 10. Application US/09261329
; Publication No. US20030092097A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Kim
; APPLICANT: Schoulen, Martin
; APPLICANT: Christiansen, Lars
; APPLICANT: Damgaard, Bo
; APPLICANT: von Delt Osten, Claus
; TITLE OF INVENTION: Cellulase Variants
; FILE REFERENCE: 48B7.204-US
; CURRENT APPLICATION NUMBER: US/09/261,329
; CURRENT FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 1013/96
; EARLIER FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Cellulase variants
; US-09-261-329-10

Query Match 72.2%; Score 39; DB 9; Length 235;
Best Local Similarity 75.0%; Pred. No. 39; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OLPQPAEL 8
Db 219 EVPGPAEL 226

RESULT 7

US 09-841-132-441

; Sequence 41. Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 21021.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OR SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SBO ID NO 441
LENGTH: 533
TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
; US-09-841-132-441

Query Match 72.2%; Score 39; DB 10; Length 533;
Best Local Similarity 70.0%; Pred. No. 95; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OLPQPAELR 10
Db 145 OLPCEAECVR 154

RESULT 8

US 09-864-761-43975

; Sequence 433975, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

Query Match 70.4%; Score 38; DB 10; Length 41;
Best Local Similarity 66.7%; Pred. No. 9.6; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LPCPBLR 10
Db 22 LPCPQDVL 30

RESULT 9

US-09-864-761-46355

; Sequence 46356, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenshang

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomico-X-1

CURRENT APPLICATION NUMBER: US/09/854 761

CURRENT FILING DATE: 2001-05-23

PRIORITY APPLICATION NUMBER: US 60/180,312

PRIORITY FILING DATE: 2000-02-04

PRIORITY APPLICATION NUMBER: US 60/207,456

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: US 09/632,366

PRIORITY FILING DATE: 2000-08-03

PRIORITY APPLICATION NUMBER: GB 24263,6

PRIORITY FILING DATE: 2000-10-04

PRIORITY APPLICATION NUMBER: US 60/236,359

PRIORITY FILING DATE: 2000-09-27

PRIORITY APPLICATION NUMBER: PCT/US01/00569

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00665

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00667

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00668

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00669

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00665

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00662

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00661

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: PCT/US01/00670

PRIORITY FILING DATE: 2001-01-30

PRIORITY APPLICATION NUMBER: US 60/234,687

PRIORITY FILING DATE: 2000-09-21

PRIORITY APPLICATION NUMBER: US 09/608,408

PRIORITY FILING DATE: 2000-06-30

PRIORITY APPLICATION NUMBER: US 09/774,203

PRIORITY FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS.: 49117

SEQ ID NO: 46356

LENGTH: 87

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: MAP TO AC007845.12

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXRESSED IN BONE MARROW, SIGNAL = 1.8

OTHER INFORMATION: EST_HUMAN HIT: AA663747.1, EVALUATE 1.00e-25

OTHER INFORMATION: SWISSPROT HIT: 061670, EVALUUE 5.00e-02

US-09-864-761-46356

Query Match 68.5%; Score 37; DB 10; Length 87;

Best Local Similarity 85.7%; Pred. No. 31; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPCPAE 7

Db 21 RLPCPAE 27

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohisen, Kari L.

APPLICANT: Ziskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: XU, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-10-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 11778

LENGTH: 284

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

Qy 2 LRPCPARLL 10

Db 211 MPVPABLL 219

RESULT 11

US-09-946-142-2

; Sequence 2, Application US/09946142

; General Information:

; Applicant: FARWICK, Mike, et al.

; Title of Invention: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE 11G02 GENE

; File Reference: 032301 WD 193

; Current Application Number: US/09/946,142

; Current Filing Date: 2001-12-28

; Number of Seq ID Nos: 2

; Software: Patentin Version 3.1

; Seq ID No: 2

; Length: 420

; Type: PRT

; Organism: Corynebacterium glutamicum

; US-09-946-142-2

Query Match 68.5%; Score 37; DB 10; Length 420;

Best Local Similarity 88.9%; Pred. No. 1.6e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLPCPAELL 9

Db 5 QLPNPAELL 13

RESULT 10
US-09-815-242-11778
Sequence 11778, Application US/09815242
; Patent No. US20020061569A1

RESULT 12

US-09-809-391-341

; Sequence 341, Application US/09809391

; Publication No. US20030049618A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 186 Human secreted proteins

; FILE REFERENCE: P2002P2

; CURRENT APPLICATION NUMBER: US/09/809, 391

; CURRENT FILING DATE: 2001-03-16

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 761

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 341

LENGTH: 106

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (53)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (80)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (96)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (102)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-809-391-341

US-09-764-868-1062

; Sequence 1062, Application US/09764868

; Patent No. US20020168711A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ32

; CURRENT APPLICATION NUMBER: US/09/764, 868

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1510

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1062

LENGTH: 118

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-955-999-71

; Sequence 71, Application US/09955999

; Publication No. US20030036505A1

; GENERAL INFORMATION:

; APPLICANT: Barish et al.

; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypep

; FILE REFERENCE: PT08CPL

; CURRENT APPLICATION NUMBER: US/09/955, 999

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/234, 997

; PRIOR FILING DATE: 2000-03-25

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 71

LENGTH: 118

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (101)

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OM protein - protein search, using sw model
Run on: July 9, 2003, 12:00:11 ; Search time 286.5 seconds
(without alignments)

22.504 Million cell updates/sec

Title: US-09-851-058-1
Perfect score: 54
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 4569144 seqs, 64473310 residues
Total number of hits satisfying chosen parameters: 4569144
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

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27: /cgn2_6/podata/1/paa/US60_COMB_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	54	100.0	471	21 US-09-791-537-104983 Sequence 104983,
2	54	100.0	471	21 US-09-791-537-143787 Sequence 143787,
3	54	100.0	476	21 US-09-791-537-143801 Sequence 143801,
4	54	100.0	476	22 US-09-801-563-43 Sequence 43, Appl
5	42	77.8	326	1 PCT-US01-4827-10106 Sequence 10106, A
6	41	75.9	50	1 PCT-US01-01354-16078 Sequence 16078, A

RESULT 1
US-09-791-537-104983
; Sequence 104983, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dancer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2003-02-22
; NUMBER OF SEQ ID NOS: 15355
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104983
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Escherichia coli

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Matches	10;	Conservative	100.0%	Pred.	No.	4	6;	Indels	0;	Gaps	0;	Sequence	16078, A	
Qy	1	QLPCPAAELLR 10										Sequence	752,	App
Db	410	QLPCPAAELLR 419										Sequence	1173,	Ap

RESULT 2
US-09-791-537-143787 ; TYPE: PRT
Sequence 143787; Application US/09791537 ; ORGANISM: Escherichia coli
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
FILE REFERENCE: 261-210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 143787
LENGTH: 471
TYPE: PRT
ORGANISM: Escherichia coli
US-09-791-537-143787
Query Match 100.0%; Score 54; DB 21; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.6; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLPCPAELLR 10
Db 410 QLCPAELLR 419
LENGTH: 476
TYPE: PRT
ORGANISM: Escherichia coli
RESULT 3
US-09-791-537-143801
Sequence 143801; Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261-210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 143801
SOFTWARE: Patentin version 3.0
SEQ ID NO 143801
LENGTH: 476
TYPE: PRT
ORGANISM: Escherichia coli
US-09-791-537-143801
Query Match 100.0%; Score 54; DB 21; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.7; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLPCPAELLR 10
Db 415 QLCPAELLR 424
LENGTH: 476
TYPE: PRT
ORGANISM: Escherichia coli
RESULT 4
US-09-801-563-43
Sequence 43; Application US/09801563
GENERAL INFORMATION:
APPLICANT: Levy, Stuart, et. al.
TITLE OF INVENTION: NMR COMPOSITIONS AND THEIR METHODS OF USE
FILE REFERENCE: PRZ-043
CURRENT APPLICATION NUMBER: US/09/801,563
CURRENT FILING DATE: 2001-03-08
PRIORITY NUMBER: 60/088,362
PRIOR APPLICATION NUMBER: 60/088,362
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 476

RESULT 5
PCT-US01-14827-10106
Sequence 10106; Application PC/TUS0114827
GENERAL INFORMATION:
APPLICANT: Huseg, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIORITY APPLICATION NUMBER: 09/577,408
PRIORITY FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 16102
SOFTWARE: Custom
SEQ ID NO 10106
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (266)..(283)
OTHER INFORMATION: Zinc finger, CCHC class domain identified by PRAM, accession
PCT-US01-14827-10106
Query Match 77.8%; Score 42; DB 1; Length 328;
Best Local Similarity 80.0%; Pred. No. 2.9e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 80.0%; 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QLPCPAELLR 10
Db 45 KLDCPAELLR 54
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 6
PCT-US01-01354-16078
Sequence 16078; Application PC/TUS0101354
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC004PCT
CURRENT APPLICATION NUMBER: PCT/US01/01354
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 42505
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16078
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (50)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01354-16078
Query Match 75.9%; Score 41; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 70; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLPCPAE 7
LENGTH: 476

Db 14 QLPCPAE 20

RESULT 7
 Sequence 16078, Application US/09764905
 US-09-764-905-16078
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PC004
 CURRENT APPLICATION NUMBER: US/09764,905
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION NUMBER: 60/179,065
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/180,628
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: 60/214,886
 PRIOR FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/217,487
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,758
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/220,963
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/217,496
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,447
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: 60/218,290
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/225,757
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/226,868
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 60/216,647
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,267
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/216,880
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,270
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/251,869
 PRIOR FILING DATE: 2000-07-08
 PRIOR APPLICATION NUMBER: 60/216,880
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: 60/234,274
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 PRIOR APPLICATION NUMBER: 60/235,834
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 PRIOR APPLICATION NUMBER: 60/224,518
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/235,369
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/228,924
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 PRIOR FILING DATE: 2000-09-14
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 PRIOR FILING DATE: 2000-09-29
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 PRIOR APPLICATION NUMBER: 60/220,964
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/241,809
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/249,299
 PRIOR FILING DATE: 2000-11-17
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 PRIOR FILING DATE: 2000-10-20
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 PRIOR FILING DATE: 2000-11-01
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 PRIOR FILING DATE: 2000-09-29
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 PRIOR FILING DATE: 2000-09-05
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 PRIOR FILING DATE: 2000-09-29
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 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/237,038
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/236,370
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/236,802
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 PRIOR APPLICATION NUMBER: 60/237,037
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/239,937
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/240,960
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/239,935
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: 60/239,937
 PRIOR FILING DATE: 2000-10-08
 PRIOR APPLICATION NUMBER: 60/241,787
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/246,474
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 PRIOR APPLICATION NUMBER: 60/241,787
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 PRIOR FILING DATE: 2000-08-14
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 PRIOR FILING DATE: 2000-08-27
 PRIOR APPLICATION NUMBER: 60/230,438
 PRIOR FILING DATE: 2000-08-06
 PRIOR APPLICATION NUMBER: 60/215,135
 PRIOR FILING DATE: 2000-08-30
 PRIOR APPLICATION NUMBER: 60/225,266
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/249,218
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,208
 PRIOR FILING DATE: 2000-11-17

Query Match 75.9%; Score 41; DB 21; Length 50;
 Best Local Similarity 100.0%; Pred. No. 70; 0; Mismatches 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-10-092-399-16078
 ; Sequence 16078, Application US/10092399
 ; GENERAL INFORMATION:
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 ; PRIOR APPLICATION NUMBER: 60/249, 213
 ; PRIOR FILING DATE: 2000/11-17
 ; PRIOR APPLICATION NUMBER: 60/249, 212
 ; PRIOR FILING DATE: 2000/11-17
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 ; PRIOR APPLICATION NUMBER: 60/231, 243
 ; PRIOR FILING DATE: 2000/09/08
 ; PRIOR APPLICATION NUMBER: 60/233, 065
 ; PRIOR FILING DATE: 2000/09/14
 ; PRIOR APPLICATION NUMBER: 60/232, 398

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 Best Local Similarity 100.0%; Pred. No. 70; 0; Mismatches 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 PCT-US00-05989-752
 ; Sequence 752, Application PCT/TUUS0005989
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; STEVE RUBEN,
 ; TITLE OF INVENTION: Human Pancreas and Pancreatic Cancer Associated Gene Sequences
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: PA105PCT
 ; CURRENT APPLICATION NUMBER: PCT/TUUS00/05989
 ; CURRENT FILING DATE: 2000-03-08
 ; EARLIER APPLICATION NUMBER: 60/124, 270
 ; EARLIER FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 928
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 752
 ; LENGTH: 78
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (72)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; PCT-US00-05989-752

Query Match 75.9%; Score 41; DB 1; Length 78;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 US-09-925-297-752
 ; Sequence 752, Application US/09925297
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA105
 ; CURRENT APPLICATION NUMBER: US/09/925, 297
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124, 270

RESULT 10
 US-09-925-297-752
 ; Sequence 752, Application US/09925297
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA105
 ; CURRENT APPLICATION NUMBER: US/09/925, 297
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124, 270

Qy 1 QLPCPAE 7
 Db 14 QLPCPAE 20

Qy 2 LPCPAELL 9
 Db 54 LPCPAELV 61

Qy 1 OLPCPAE 7
 Db 14 OLPCPAE 20

RESULT 8
 US-10-092-399-16078
 ; Sequence 16078, Application US/10092399
 ; GENERAL INFORMATION:

PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 928
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 752
 LENGTH: 78
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (72)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-09-925-301-1173

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Oy	41	23	78	75.9%	87.5%	1.1e+02	0	0	0
Db	9	61							

RESULT 11
 Sequence 1173 Application PC/TUS0005882
 GENERAL INFORMATION:
 APPLICANT: Craig Rosen,
 APPLICANT: Steve Ruben,
 TITLE OF INVENTION: Human Cancer Associated Gene Sequences and Polypeptides
 FILE REFERENCE: PAX106PCT
 CURRENT APPLICATION NUMBER: PCT/US00/05882
 CURRENT FILING DATE: 2000-03-08
 EARLIER APPLICATION NUMBER: 60/124,270
 EARLIER FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1694
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 1173
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (171)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 PCT-US00-05882-1173

Query Match

Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	
Oy	41	1	180	75.9%	87.5%	2.4e+02	0	0	0
Db	9	31							

RESULT 13
 Sequence 22, Application PC/TUS0231095
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: AZIMAI, Yalda
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: BBCHA, Shanya D.
 APPLICANT: BOROWSKY, Mark L.
 APPLICANT: CHAWLA, Narinder K.
 APPLICANT: ELLIOTT, Vicki S.
 APPLICANT: EMERLING, Brooke M.
 APPLICANT: GANDHI, Ameena R.
 APPLICANT: GIETZEN, Kimberly J.
 APPLICANT: GORVAD, Ann E.
 APPLICANT: GRIFFIN, Jennifer A.
 APPLICANT: HAFALIA, April J.A.
 APPLICANT: ISON, Craig H.
 APPLICANT: KABLE, Amy E.
 APPLICANT: KALAFUS, Daniel P.
 APPLICANT: LEHR-MASON, Patricia M.
 APPLICANT: LU, Dyung Anna M.
 APPLICANT: MARQUIS, Joseph P.
 APPLICANT: NGUYEN, Daniel B.
 APPLICANT: RAMKUMAR, Jayalaxmi
 APPLICANT: RICHARDSON, Thomas W.
 APPLICANT: SAPPERSTEIN, Stephanie K.
 APPLICANT: SHARRAKAR, Anita
 APPLICANT: TANG, Y. Tom
 APPLICANT: TERN, Uyen K.
 APPLICANT: WARREN, Bridget A.
 APPLICANT: XU, Yuming
 APPLICANT: YAO, Monique G.
 APPLICANT: YUE, Rubin
 APPLICANT: YUE, Henry
 APPLICANT: YUE, Henry
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEA
 CURRENT APPLICATION NUMBER: PCT/US02/31095
 CURRENT FILING DATE: 2002-03-26
 FILE REFERENCE: PF-123 PCT
 CURRENT APPLICATION NUMBER: PCT/US02/31095
 PRIOR APPLICATION NUMBER: US 60/326,389
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US 60/327,380
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: US 60/328,186
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: US 60/329,690
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/345,384
 PRIOR FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: US 60/348,165
 PRIOR FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: US 60/350,219
 PRIOR FILING DATE: 2001-11-02
 PRIOR APPLICATION NUMBER: US 60/344,518
 PRIOR FILING DATE: 2001-11-09
 PRIOR APPLICATION NUMBER: US 60/345,143
 PRIOR FILING DATE: 2001-11-09

RESULT 12
 Sequence 1173 Application US/09925301
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA106
 CURRENT APPLICATION NUMBER: US/09/925,301
 CURRENT FILING DATE: 2001-03-10
 PRIOR APPLICATION NUMBER: PCT/US00/05882
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1694
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 1173
 LENGTH: 180
 TYPE: PRT

PRIOR APPLICATION NUMBER: US 60/332,375
 PRIOR FILING DATE: 2001-11-16
 Remaining prior application data removed - see File wrapper or PALM.
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: PERL Program
 SEQ ID NO: 22
 LENGTH: 412
 TYPE: PRT
 FEATURE:
 ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No: 7503812CD1
 PCT-US02-31055-22

Query Match 75.9%; Score 41; DB 1; Length 412;
 Best Local Similarity 87.5%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; SEQ ID NO: 22
 Qy 2 LPCPPELL 9
 Db 256 LPCPABELV 263

RESULT 14
 PCT-US02-19669-296
 Sequence 296, Application PC/TUS0219669
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc. et al.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
 TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
 FILE REFERENCE: MRI-038PC
 CURRENT APPLICATION NUMBER: PCT/US02/19669
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: US 60/299,887
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/301,572
 PRIOR FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: US 60/305,501
 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 60/325,002
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/362,585
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/xxx,xxx
 PRIOR FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 296
 LENGTH: 445
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US02-19669-296

RESULT 15
 US-08-601-814-6
 Sequence 6, Application US/08691014
 GENERAL INFORMATION:
 APPLICANT: Rio, Marie-Christine
 APPLICANT: Tomassotto, Catherine
 APPLICANT: Basser, Paul
 APPLICANT: Byrne, Jennifer
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
 TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
 NUMBER OF SEQUENCES: 73
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 75.9%; Score 41; DB 1; Length 445;
 Best Local Similarity 87.5%; Pred. No. 5.6e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; SEQ ID NO: 22
 Qy 2 LPCPABELV 9
 Db 289 LPCPABELV 296

Search completed: July 9, 2003, 12:13:15
 Job time : 289.5 secs

ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0. Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/691,814
 FILING DATE: 31-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/002,183
 FILING DATE: 09-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1383.0090001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2543
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 415 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-691-814-6

Query Match 75.9%; Score 41; DB 10; Length 445;
 Best Local Similarity 87.5%; Pred. No. 5.6e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; SEQ ID NO: 22
 Qy 2 LPCPABELV 9
 Db 289 LPCPABELV 296

Run on: July 9, 2003, 12:00:51 ; Search time 94.5 Seconds
 (without alignments)
 27.740 Million cell updates/sec

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GenFore version 5.1.6

OM protein - protein search, using sw model

Database	Title:	Perfect score:	Scoring table:	Searched:	Total number of hits satisfying chosen parameters:	Minimum DB seq length:	Maximum DB seq length:	Post-processing:
	US-09-851-058-1	54	BLOSUM62 gapop 10.0 , Gapext 0.5	1221054 seqs, 262139423 residues	1221054	0	200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending Patents_AA_New: *

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	54	100.0	10	PCT-US02-14369-1	Sequence 1, Application PCT-US02-14369-1
2	54	100.0	10	US-09-851-058-1	Sequence 1, Application PCT-US02-14369-1
3	54	100.0	471	US-10-254-763-12	Sequence 12, Application PCT-US02-14369-1
4	83.3	79	79	PCT-US02-3272-20678	Sequence 20678, Application PCT-US02-3272-20678
5	83.3	79	10	US-09-978-825-20678	Sequence 20678, Application PCT-US02-3272-20678
6	83.3	79	12	US-10-057-498-20678	Sequence 20678, Application PCT-US02-3272-20678
7	77.8	118	12	US-10-437-963-127901	Sequence 127901, Application PCT-US02-14369-1
8	77.8	431	12	US-09-437-963-103514	Sequence 103514, Application PCT-US02-14369-1
9	75.9	176	10	US-09-724-676-57238	Sequence 57238, Application PCT-US02-14369-1
10	75.9	176	10	US-09-724-676-57238	Sequence 57238, Application PCT-US02-14369-1
11	75.9	186	10	US-09-724-676-57248	Sequence 57248, Application PCT-US02-14369-1
12	75.9	186	10	US-09-724-676-57248	Sequence 57248, Application PCT-US02-14369-1
13	75.9	223	10	US-09-724-676-57240	Sequence 57240, Application PCT-US02-14369-1
14	75.9	223	10	US-09-724-676-57240	Sequence 57240, Application PCT-US02-14369-1
15	75.9	233	10	US-09-724-676-57239	Sequence 57239, Application PCT-US02-14369-1
16	75.9	233	10	US-09-724-676-57239	Sequence 57239, Application PCT-US02-14369-1
17	75.9	435	10	US-09-724-676-57242	Sequence 57242, Application PCT-US02-14369-1
18	75.9	435	10	US-09-724-676-57242	Sequence 57242, Application PCT-US02-14369-1
19	75.9	442	10	PCT-US02-19669A-296	Sequence 296, Application PCT-US02-19669A-296

ALIGNMENTS

SEQ ID NO	TYPE: PRT	ORGANISM: Artificial sequence
1	FEATURE: OTHER INFORMATION: synthetic peptides	PCT-US02-14369-1
2	Query Match	100.0%; Score 54; DB 2
3	Best Local Similarity	100.0%; Pred. No. 0.022
4	Matches	10; Conservative 0; Mismatches 0
5	QY	1 QLPCPAELLR 10
6	Db	1 QLPCPAELLR 10

RESULT 2

US-09-851-058-1

GENERAL INFORMATION:

- APPLICANT: Parker, Kenneth
- APPLICANT: Nadler, Timothy
- APPLICANT: Smolka, Marcus
- APPLICANT: Vella, George
- APPLICANT: Huang, Yulin
- APPLICANT: Abersold, Rudolf

GENERAL INFORMATION:

- APPLICANT: Parker, Kenneth
- APPLICANT: Nadler, Timothy
- APPLICANT: Smolka, Marcus
- APPLICANT: Vella, George
- APPLICANT: Huang, Yulin
- APPLICANT: Abersold, Rudolf

APPLICANT: Smolka, Marcus
 TITLE OF INVENTION: Process for Analyzing Protein Samples
 FILE REFERENCE: SPP-172
 CURRENT APPLICATION NUMBER: US/09/851,058
 CURRENT FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 3
 SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptides
 US-09-851-058-1

Query Match 100.0%; Score 54; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.022; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QLPCPAELLR 10
 Db 1 QLPCPAELLR 10

RESULT 3
 US-10-254-763-12

; Sequence 12, Application US/10254763
 ; GENERAL INFORMATION:

; APPLICANT: TAKAGI, HIROSHI
 ; APPLICANT: WADA, MASARU
 ; APPLICANT: NAKAMORI, SHIGERU
 ; TITLE OF INVENTION: L-Cysteine-Producing Bacterium and Method for Producing L-Cysteine
 ; FILE REFERENCE: 22854US0
 ; CURRENT APPLICATION NUMBER: US/10/254,763
 ; CURRENT FILING DATE: 2003-01-06
 ; PRIOR APPLICATION NUMBER: JP 2001-302008
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO: 12
 ; LENGTH: 471
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-10-254-763-12

Query Match 100.0%; Score 54; DB 12; Length 471;
 Best Local Similarity 100.0%; Pred. No. 0.76; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QLPCPAELLR 10
 Db 410 QLPCPAELLR 419

RESULT 4
 PC1-US02-32727-20678

; Sequence 20678, Application PC/TUS0232727
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skelley, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Bhattia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Sining
 ; APPLICANT: Jen, Shyian
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darrin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Barth, Brenda
 ; APPLICANT: Douglass, John
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514C1
 ; CURRENT APPLICATION NUMBER: US/09/978,825
 ; CURRENT FILING DATE: 2003-01-29
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 20678
 ; LENGTH: 79
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 ; US-09-978-825-20678

RESULT 5
 US-09-978-825-20678

; Sequence 20678, Application US/09978825
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skelley, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Bhattia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Sining
 ; APPLICANT: Jen, Shyian
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darrin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Barth, Brenda
 ; APPLICANT: Douglass, John
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514C1
 ; CURRENT APPLICATION NUMBER: US/09/978,825
 ; CURRENT FILING DATE: 2003-01-29
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 20678
 ; LENGTH: 79
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 ; US-09-978-825-20678

RESULT 6
 US-10-057498-20678

; Sequence 20678, Application US/10057498
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skelley, Yasir
 ; APPLICANT: Persing, David
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514
 ; CURRENT APPLICATION NUMBER: US/10/057,498
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 29212
 ; SEQ ID NO 20678
 ; LENGTH: 79
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 ; US-09-978-825-20678

US-10-057-498-20678

Query Match 83.3%; Score 45; DB 12; length 79;

Best Local Similarity 88.9%; Pred. No. 4.6; 0; Mismatches 8; Conservative 0; Indels 1; Gaps 0; Gaps 0;

Qy 2 LPCPELLR 10
Db 54 LPCPELLR 62

RESULT 7

US-10-437-963-127901
Sequence 127901, Application US/10437963

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437, 963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 127901
LENGTH: 118

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_100936C.1.pep

US-10-437-963-127901

Query Match 77.8%; Score 42; DB 12; length 118;
Best Local Similarity 77.8%; Pred. No. 21; 1; Mismatches 7; Conservative 1; Indels 0; Gaps 0;Qy 14 LPCPAILR 10
Db 14 LPCPAILR 22

RESULT 8

US-10-437-963-103514
Sequence 103514, Application US/10437963

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437, 963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 103514
LENGTH: 431

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

NAME/KEY: unsure

LOCATION: (1).(.431)

OTHER INFORMATION: unsure at all xaa locations

FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_100936C.1.pep
; US-10-437-963-103514Query Match 77.8%; Score 42; DB 12; Length 431;
Best Local Similarity 80.0%; Pred. No. 69; 0; Mismatches 8; Conservative 0; Indels 2; Gaps 0; Gaps 0;Qy 1 QLPCPAELLR 10
Db 32 QLPCPENLR 41

RESULT 9

US-09-724-676-57238
Sequence 57238, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724, 676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SEQ ID NO 57238
LENGTH: 176

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-57238
Query Match 75.9%; Score 41; DB 10; Length 176;
Best Local Similarity 87.5%; Pred. No. 45; 0; Mismatches 7; Conservative 1; Indels 0; Gaps 0; Gaps 0;Qy 2 LPCPAELL 9
Db 30 LPCPAELV 37

RESULT 10

US-09-724-676A-57238
Sequence 57238, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724, 676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SEQ ID NO 57238
LENGTH: 176

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-57238
Query Match 75.9%; Score 41; DB 10; Length 176;
Best Local Similarity 87.5%; Pred. No. 45; 0; Mismatches 7; Conservative 1; Indels 0; Gaps 0; Gaps 0;Qy 2 LPCPAELL 9
Db 30 LPCPAELV 37

RESULT 11

US-09-724-676-57248
Sequence 57248, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724, 676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 57248
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676-57248

Query Match 75.9%; Score 41; DB 10; Length 186;
; Best Local Similarity 87.5%; Pred. No. 47;
; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 2 LPCPAELL 9
; Db 30 LPCPAELV 37

RESULT 12

US-09-724-676A-57248

Sequence 57248, Application US/09/724676A
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181_4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 57248
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676A-57248

Query Match 75.9%; Score 41; DB 10; Length 186;

Best Local Similarity 87.5%; Pred. No. 47;
; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 2 LPCPAELL 9
; Db 30 LPCPAELV 37

RESULT 15

US-09-724-676-57239

Sequence 57239, Application US/09/724676
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181_4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 57239
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676-57239

Query Match 75.9%; Score 41; DB 10; Length 233;

Best Local Similarity 87.5%; Pred. No. 58;
; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 2 LPCPAELL 9
; Db 77 LPCPAELV 84

Search completed: July 9, 2003, 12:16:30
Job time: 95.5 secs

Query Match 75.9%; Score 41; DB 10; Length 223;
; Best Local Similarity 87.5%; Pred. No. 55;
; Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; Qy 2 LPCPAELL 9
; Db 77 LPCPAELV 84
; ORGANISM: Homo sapiens
; US-09-724-676-57240

RESULT 14
; US-09-724-676A-57240
; Sequence 57240, Application US/09/724676A
; GENERAL INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Search time 18.5 Seconds
(without alignments)
51.965 Million cell updates/sec

Total number of hits satisfying chosen parameters: 283224

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*

1: pirl1;*
2: pin2;*
3: pi3;*
4: pirk;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	54	100	0	WZEC
2	54	100	0	tryptophanase (EC 4.1.99.1) - Escherichia coli (strain K-12)
3	54	100	0	C;Species: Escherichia coli
4	47	87	9	C;Date: 14-Nov-1983 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002
5	41	75	9	C;Accession: E65173; A91789; I41097; I65358; A01136
6	41	75	9	R;Blattner, F.R.;Junkett, III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
7	40	74	1	Science 277, 1453-1462, 1997
8	39	72	2	A;Title: The complete genome sequence of Escherichia coli K-12.
9	39	72	2	A;Reference number: A64720; MUID:97426617; PMID:9278503
10	39	72	2	A;Accession: E65173
11	39	72	2	A;Status: nucleic acid sequence not shown; translation not shown
12	39	72	2	A;Molecule type: DNA
13	38	70	4	A;Residues: 1-476 <BLAT>
14	37	68	5	A;Experimental source: strain K-12, substrain MG1655
15	36	66	7	A;Cross-references: GB:AE004448; GB:U00096; NID:91790142; PIDN:AACT76731.1; PID:91790142
16	36	66	7	A;Reference number: R64720; MUID:82007678; PMID:6288608
17	36	66	7	A;Accession: A91789
18	36	66	7	A;Molecule type: DNA
19	36	66	7	A;Residues: 6-141,'T',143,'OG',146-393,'TG',386-476 <DEE>
20	35	64	8	A;Experimental source: strain K-12
21	35	64	8	A;Note: the authors translated the codons GAT, ACG, and CAG for residues 142, 144, and 145.
22	35	64	8	R;Kogayama, H.; Matsubara, H.; Snell, E.E.
23	35	64	8	J. Biol. Chem. 247, 1576-1586, 1972
24	35	64	8	A;Title: The chemical structure of tryptophanase from Escherichia coli. III. Isolation and characterization of the tryptophanase from Escherichia coli. J. Biol. Chem. 247, 1576-1586, 1972
25	34	63	0	A;Reference number: A92100; MUID:72134434; PMID:4551944
26	34	63	0	A;Contents: annotation: sequences of tryptic peptides; strain K-12
27	34	63	0	A;Note: Lys-275 binds pyridoxal 5'-phosphate
28	34	63	0	R;Tokushige, M.; Tsujimoto, N.; Oda, T.; Honda, T.; Yumoto, N.; Ito, S.; Yamamoto, M.
29	34	63	0	Biochimie 71, 711-720, 1989
30	34	63	0	A;Title: Role of cysteine residues in tryptophanase for monovalent cation-induced activation
31	34	63	0	A;Reference number: I41097; MUID:89323226; PMID:2502187
32	34	63	0	A;Accession: I41097
33	34	63	0	A;Molecule type: DNA
34	34	63	0	A;Molecule type: DNA
35	34	63	0	A;Cross-references: EMBL:EMBL/DBDJ
36	34	63	0	A;Status: translated from GB/EMBL/DDJB
37	34	63	0	A;Molecule type: DNA
38	34	63	0	A;Residues: 6-27 <RS2>
39	34	63	0	A;Cross-references: GB:M11990; NID:9147999; PIDN:AAA24679.1; PID:9148001
40	34	63	0	C;Genetics:
41	34	63	0	A;Gene: tnaA

ALIGNMENTS

Result No.	Score	Query Length	DB ID	Description
1	54	0	WZEC	tryptophanase (EC 4.1.99.1) - Escherichia coli (strain K-12)
2	476	1	E91209	C;Species: Escherichia coli
3	476	2	H86055	C;Date: 14-Nov-1983 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002
4	476	2	B82492	C;Accession: E65173; A91789; I41097; I65358; A01136
5	476	2	I38244	R;Blattner, F.R.;Junkett, III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
6	468	2	S47447	Science 277, 1453-1462, 1997
7	5149	2	F83345	A;Title: The complete genome sequence of Escherichia coli K-12.
8	72	2	S1052	A;Reference number: A64720; MUID:97426617; PMID:9278503
9	72	2	A32244	A;Accession: E65173
10	72	2	A43584	A;Status: nucleic acid sequence not shown; translation not shown
11	547	1	D71515	A;Molecule type: DNA
12	553	2	D71515	A;Residues: 6-141,'T',143,'OG',146-393,'TG',386-476 <DEE>
13	642	2	E87644	A;Experimental source: strain K-12
14	284	5	F83615	A;Note: the authors translated the codons GAT, ACG, and CAG for residues 142, 144, and 145.
15	66	7	G84331	R;Kogayama, H.; Matsubara, H.; Snell, E.E.
16	335	2	I25054	J. Biol. Chem. 247, 1576-1586, 1972
17	339	2	I25054	A;Title: The chemical structure of tryptophanase from Escherichia coli. III. Isolation and characterization of the tryptophanase from Escherichia coli. J. Biol. Chem. 247, 1576-1586, 1972
18	415	2	E83281	A;Reference number: A92100; MUID:72134434; PMID:4551944
19	976	2	C84508	A;Contents: annotation: sequences of tryptic peptides; strain K-12
20	118	2	T32922	A;Note: Lys-275 binds pyridoxal 5'-phosphate
21	146	2	T80304	R;Tokushige, M.; Tsujimoto, N.; Oda, T.; Honda, T.; Yumoto, N.; Ito, S.; Yamamoto, M.
22	281	2	B85279	Biochimie 71, 711-720, 1989
23	590	2	T45672	A;Title: Role of cysteine residues in tryptophanase for monovalent cation-induced activation
24	832	2	S176815	A;Reference number: I41097; MUID:89323226; PMID:2502187
25	141	2	T33212	A;Accession: I41097
26	196	2	A46623	A;Molecule type: DNA
27	206	2	D98630	A;Cross-references: GB:M11990; NID:9147999; PIDN:AAA24679.1; PID:9148001
28	206	2	D85481	C;Genetics:
29	222	2	A55263	A;Gene: tnaA

A;Map position: 83 min
 C;Complex: homotetramer
 C;Function:
 C;Description: catalyses the degradation of tryptophan to indole, pyruvate, and ammonia;
 C;Keywords: carbon-carbon lyase; homotetramer

RESULT 2
 E91209
 tryptophanase (imported) - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;Accession: E91209
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 qnsawara, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 A;Residues: 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gene
 A;Reference number: A99629; MUID:2115631; PMID:11258796
 A;Accession: E91209
 A;Molecule type: DNA
 A;Residues: 1-475 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BAB30608.1; PID:913364120; GSPDB:GN00154
 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
 A;Genetics:
 A;Gene: E9c4645
 C;Superfamily: tryptophanase

Query Match 100.0%; Score 54; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.055; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 HB0555
 tryptophanase [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: HB0555
 R;Perne, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamakis, K.; Apodaca, N.; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-476 <STOP>
 A;Cross-references: GB:AE005174; PIDN:912518553; PIDN:AGG58908.1; GSPDB:GN00145; UMGp:252
 C;Genetics:
 C;Gene: tnaA
 C;Superfamily: tryptophanase

Query Match 100.0%; Score 54; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.055; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPCPAELLR 10

Db 415 QLPCPAELLR 424

RESULT 4
 B82492
 tryptophanase VCA0161 [imported] - vibrio cholerae (strain N16961 serogroup O1)
 C;Species: vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: B82492
 R;Heideleberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. charlson, D.; Brzuska, M.D.; Yamashita, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: B82492
 A;Map position: 2
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-472 <HET>
 A;Cross-references: GB:AE004357; GB:AE003953; NID:99657547; PIDN:AAF96074.1; GSPDB:GN 04357
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCA0161
 A;Map position: 2
 A;Superfamily: tryptophanase

Query Match 87.0%; Score 47; DB 2; Length 472;
 Best Local Similarity 90.0%; Pred. No. 0.96; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLPCPAELLR 10

Db 410 QHPCPAELLR 419

RESULT 5
 138027
 MLN 64 Protein - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Nov-1999
 C;Accession: 138027; S60682
 R;Romasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lideureau, Genomics 28, 367-376, 1995
 A;Title: Identification of four novel human genes amplified and overexpressed in breast cancer
 A;Reference number: 137080; MUID:96039245; PMID:7490069
 A;Accession: 138027
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-445 <RRES>
 A;Cross-references: EMBL:X80198; NID:9951278; PIDN:CAA56489.1; PID:9951279
 A;Note: submitted to the EMBL Data Library, July 1994
 C;Genetics:
 A;Gene: MLN64

Query Match 75.9%; Score 41; DB 2; Length 445;
 Best Local Similarity 87.5%; Pred. No. 11; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LQLPCPAELL 9

Db 289 LQLPCPAELL 296

RESULT 6
 S47447
 hypothetical protein YML102w - yeast (*Saccharomyces cerevisiae*)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 26-May-2000
 C;Accession: S47447
 R;Barrell, B.G.
 submitted to the EMBL Data Library, August 1994
 A;Reference number: S47447

Qy

A; Molecule type: DNA
A; Residues: 1-468
A; Cross-references: EMBL:X80835; NID:9530339; PIDN:CAA56795_1; PID:9530342; MIPS:YML102w
C; Genetics:
A; Gene: SGD:CAC2
A; Cross-references: SGD:S0004570; MIPS:YML102w
A; Map position: 13I.
C; Superfamily: unassigned WD repeat proteins; WD repeat homology
Query Match 75.9%; Score 41; DB 2; Length 468;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QLPCPABLR 10
Db 237 :||| :||| ELPCPGSDVLR 246

RESULT 7
R8345
Probable non-ribosomal peptide synthetase PA2402 [imported] - *Pseudomonas aeruginosa* (st
C; Species: *Pseudomonas aeruginosa*
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: F8345
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mikoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A; Reference number: A82950; MID:20437337; PMID:10984043
A; Accession: F8345
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-5149 <STO>
A; Cross-references: GB:AG04667; GB:AE004091; NID:9948444; PIDN:AAG05790_1; GSPDB:GN001
C; Genetics:
A; Gene: PA2402
C; Superfamily: acyl carrier protein homology; acetate-CoA ligase homology
C; Keywords: carrier protein; phosphopantetheine; phosphoprotein
F; 1015-1032/Domain: acyl carrier protein homology <ACP1>
F; 2034-2179/Domain: acetate-CoA ligase homology <ACLL2>
F; 2456-2504/Domain: acyl carrier protein homology <ACCL3>
F; 3034-3525/Domain: acetyl carrier protein homology <ACP3>
F; 4503-5040/Domain: acetate-CoA ligase homology <ACL4>
F; 5037-5125/Domain: acyl carrier protein homology <ACP4>
F; 1047-2528,3573,5089/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
Query Match 74.1%; Score 40; DB 2; Length 5149;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QLPCPABLR 10
Db 2098 RLPCPABLR 2107

RESULT 8
R82730
ribonuclease HII XYL1041 [Imported] - *Xylella fastidiosa* (strain 9a5c)
C; Species: *Xylella fastidiosa*
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C; Accession: H82730
R; anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A; Reference number: A82215; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: H82730
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-468

RESULT 9
S10527
endo-glucanase_B precursor - *Pseudomonas fluorescens*
C; Species: *Pseudomonas fluorescens*
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C; Accession: S10527
R; Gilbert, H.J.; Hall, J.; Hazelwood, G.P.; Ferreira, L.M.A.
Mol. Microbiol. 4, 759-767, 1990
A; Title: The N-terminal region of an endoglucanase from *Pseudomonas fluorescens* subsp
A; Reference number: S10527; MID:9035536; PMID:2117693
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-511 <CIL>
A; Cross-references: EMBL:X52615; NID:945497; PIDN:CAA36844_1; PID:945498
C; Superfamily: bacterial cellulose-binding domain homology; glycosidase GWGW domain h
F; 31-128/Domain: bacterial cellulose-binding domain homology <BCB>
F; 180-217/Domain: glycosidase GWGW domain homology <WG>
F; 32-127/disulfide bonds: #status predicted
Query Match 72.2%; Score 39; DB 2; Length 511;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QLPCPAEL 8
Db 485 EVPCPAEL 492

RESULT 10
A32244
60K cysteine-rich outer membrane protein 2 precursor, serotype L1 and L2 - *Chlamydia*
C; Species: *Chlamydia trachomatis*
C; Date: 12-Oct-1998 #sequence_revision 27-Jun-1994 #text_change 16-Jul-1999
C; Accession: A32244; A3584; A36043; A310472; JT0419; S18981; S24277
R; Allen, J.E.; Stephens, R.S.
J. Bacteriol. 171, 285-291, 1989
A; Title: Identification by sequence analysis of two-site posttranslational processing
A; Reference number: A32244; MID:89123030; PMID:2914847
A; Accession: A32244
A; Molecule type: DNA
A; Residues: 1-547 <CALL>
A; Cross-references: GB:M23001; NID:9144552; PIDN:AAA23152_1; PID:9144553

A;Experimental source: strain L2/434/Bu
A;Note: parts of this sequence, including the amino ends of the precursor and mature pro
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1195-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton
A;Accession: A43584; MUID:91147205; PMID:1997423
A;Residues: 1-547
A;Molecule type: DNA
A;Cross-references: GB:M23001; NID:9144552; PIDN:AAA23152.1; PID:9144553
A;Experimental source: serovar 2, strain L2/434/Bu
A;Title: General colorimetric method for DNA diagnostics allowing direct solid-phase gen
A;Reference number: A36043; MUID:90370827; PMID:2118652
A;Accession: A36043
A;Molecule type: DNA
A;Residues: 294-402 <WAT>
R;Lambden, P.R.; Everson, J.S.; Ward, M.E.; Clarke, I.N.
Gene 87, 105-112, 1990
A;Cross-references: GB:M35148; GB:M23180; GB:M35161; NID:9144485
A;Experimental source: serotype L1
R;Clarke, I.N.; Ward, M.E.; Lambden, P.R.
Gene 71, 307-314, 1988
A;Experimental source: serotype L1
A;Title: Molecular cloning and sequence analysis of a developmentally regulated cysteine
A;Reference number: J70419; MUID:89138006; PMID:3066701
A;Accession: J70419
A;Molecule type: DNA
A;Residues: 1-547 <CL>>
A;Cross-references: GB:M35148; NID:9144485; PIDN:AAA23119.1; PID:9144487
A;Experimental source: serotype L1
A;Gene: omp2; omcB
C;Function:
A;Description: associated with differentiation of reticulate bodies into elementary bod
C;Superfamily: 60K cysteine-rich outer membrane protein
C;Keywords: membrane protein; virulence
F;1-22/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: propeptide #status experimental <PRO>
F;41-547/Product: 60K cysteine rich outer membrane protein 2 #status predicted <MAT>
A;Cross-references: GB:AE001317; GB:AE001317; NID:93328863; PIDN: AAC6042.1; PID:9332
A;Experimental source: serotype D, strain UW-3/CX
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1195-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton
A;Accession: C43584; MUID:91147205; PMID:1997423
A;Molecule type: DNA
A;Residues: 7-238, 240-553
A;Cross-references: GB:X53388; NID:940760; PIDN:CAA38257.1; PID:940761
A;Experimental source: serotype C
R;Watson, M.W.; Lambden, P.R.; Ward, M.E.; Clarke, I.N.
FEMS Microbiol. Lett. 65, 293-297, 1989
A;Title: Chlamydia trachomatis 60 kDa cysteine rich outer membrane protein: sequence
A;Reference number: A43584; MUID:91147205; PMID:1997423
A;Accession: C43584
A;Molecule type: DNA
A;Residues: 7-553 <WAT>
A;Cross-references: EMBL:X53510; NID:940681; PIDN:CAA37588.1; PID:940683
A;Experimental source: serotype B
C;Genetics:
A;Gene: omp2; omcB
C;Function:
A;Description: associated with differentiation of reticulate bodies into elementary b
A;Note: essential for the structural integrity of the outer envelope of the elementary
C;Superfamily: 60K cysteine-rich outer membrane protein
C;Keywords: membrane protein; virulence
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-46/Domain: propeptide #status predicted <PRO>
F;47-553/Product: 60K cysteine-rich outer membrane protein 2 #status predicted <MAT>
R;Coles, A.M.; Allan, I.; Pearce, J.H.
Query Match 72.2%; Score 39; DB 1; Length 547;
Best Local Similarity 70.0%; Pred. No. 29; No. 29;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QLRCPAAELIR 10
Db 139 QLPCEAEFVR 148
RESULT 12
D71515 60K cysteine-rich outer membrane protein 2 precursor serotypes B, C, and D - Chlamydi
;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 20-Aug-1999
C;Accession: D71515; C43584; S11673
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: D71515
A;Molecule type: DNA
A;Residues: 1-553 <ARN>
A;Cross-references: GB:AE001317; GB:AE001317; NID:93328863; PIDN: AAC6042.1; PID:9332
A;Experimental source: serotype D, strain UW-3/CX
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1195-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton
A;Accession: C43584; MUID:91147205; PMID:1997423
A;Molecule type: DNA
A;Residues: 7-238, 240-553
A;Cross-references: GB:X53388; NID:940760; PIDN:CAA38257.1; PID:940761
A;Experimental source: serotype C
R;Watson, M.W.; Lambden, P.R.; Ward, M.E.; Clarke, I.N.
FEMS Microbiol. Lett. 65, 293-297, 1989
A;Title: Chlamydia trachomatis 60 kDa cysteine rich outer membrane protein: sequence
A;Reference number: S11673
A;Accession: S11673
A;Molecule type: DNA
A;Residues: 7-553 <WAT>
A;Cross-references: EMBL:X53510; NID:940681; PIDN:CAA37588.1; PID:940683
A;Experimental source: serotype B
C;Genetics:
A;Gene: omp2; omcB
C;Function:
A;Description: associated with differentiation of reticulate bodies into elementary b
A;Note: essential for the structural integrity of the outer envelope of the elementary
C;Superfamily: 60K cysteine-rich outer membrane protein
C;Keywords: membrane protein; virulence
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-46/Domain: propeptide #status predicted <PRO>
F;47-553/Product: 60K cysteine-rich outer membrane protein 2 #status predicted <MAT>
Query Match 72.2%; Score 39; DB 2; Length 553;

Best Local Similarity 70.0%; Pred. No. 29; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

E8764 sensory box histidine kinase/response regulator [Imported] - Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: E8764

R;Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Brinkman, F.S.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolonay, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-442 <STOP>

A;Cross-references: GB:AE005673; NID:913424865; PIDN:AAK25153.1; GSDB:GN00148

A;Gene: CC3191

Query Match 70.4%; Score 38; DB 2; Length 642;

Best Local Similarity 100.0%; Pred. No. 51; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CPAELLR 10

Db 340 CPAELLR 346

RESULT 14

F83615 hypothetical protein PA0244 [Imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: F83615

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Breaker, R.A.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: F83615

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-284 <STOP>

A;Cross-references: GB:AE004462; GB:AE004091; NID:99946077; PIDN:AAG03633.1; GSDB:GN001

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA0244

C;Superfamily: shikimate dehydrogenase; shikimate dehydrogenase homology

Query Match 68.5%; Score 37; DB 2; Length 284;

Best Local Similarity 77.8%; Pred. No. 36; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LPCPAELLR 10

Db 211 MPVPAELLR 219

RESULT 15

G84331 hypothetical Protein Wng1800h [Imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:55:50 ; Search time 15.5 Seconds
(without alignments)
26.759 Million cell updates/sec

Title: US-09-851-058-1

Perfect score: 54

Sequence: 1 QLPCPAELLR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	RESULT 1
1	54	100.0	471	1 TNAA_ECOLI	08xb34 escherichia	TNAA_ECOLI
2	54	100.0	471	1 TNAA_ECOLI	P00513 escherichia	TNAA_ECOLI
3	54	100.0	471	1 TNAA_HAEIN	09c127 pasteurella	TNAA_HAEIN
4	54	100.0	472	1 TNAA_VIBCH	007674 haemophilus	TNAA_VIBCH
5	47.0	87.0	445	1 ML64_HUMAN	09k0105 vibrio chol	ML64_HUMAN
6	41	75.9	446	1 ML64_MOUSE	014449 homo sapien	ML64_MOUSE
7	41	75.9	446	1 CAC2_YEAST	061142 mus musculus	CAC2_YEAST
8	41	75.9	468	1 RNN2_XYLFA	004199 saccharomyces	RNN2_XYLFA
9	39	72.2	234	1 GUNB_PSEFL	08ps17 xylorella fas	GUNB_PSEFL
10	39	72.2	511	1 OM6C_CHLTR	P18c26 pseudomonas	OM6C_CHLTR
11	39	72.2	547	1 P26758	P26758 chlamydia t	P26758
12	39	72.2	547	1 P1851	P1851 chlamydia t	P1851
13	39	72.2	547	1 P23003	P23003 chlamydia t	P23003
14	39	72.2	547	1 OM6L_CHLTR	P21354 chlamydia t	OM6L_CHLTR
15	38	70.4	632	1 STC_CLOBE	P26047 clostridium	STC_CLOBE
16	37	68.5	547	1 NH35_HUMAN	014771 homo sapien	NH35_HUMAN
17	37	68.5	578	1 YAF9_SCHPO	017771 caenorhabdi	YAF9_SCHPO
18	36	66.7	339	1 TM61_MOUSE	009862 schizosacch	TM61_MOUSE
19	35	66.7	370	1 TXM1_HUMAN	P58749 mus musculus	TXM1_HUMAN
20	36	66.7	398	1 P03435	043435 homo sapien	P03435
21	35	64.8	213	1 GUN5_HUMAN	P43116 humicola in	GUN5_HUMAN
22	35	64.8	257	1 IDLC_HUMAN	014445 homo sapien	IDLC_HUMAN
23	34	63.0	196	1 RTGK_ECOLT	P28897 escherichia	RTGK_ECOLT
24	34	63.0	222	1 TSN2_HUMAN	060336 homo sapien	TSN2_HUMAN
25	34	63.0	268	1 DUT_PRVKA	090030 pseudorabies	DUT_PRVKA
26	34	63.0	412	1 YM04_ARCFU	028079 archaeoglob	YM04_ARCFU
27	34	63.0	519	1 TRPE_SERMA	P00597 secratia ma	TRPE_SERMA
28	34	63.0	556	1 OM6_CHLPR	P23100 chlamydia p	OM6_CHLPR
29	34	63.0	825	1 I14R_HUMAN	P24394 hom sapien	I14R_HUMAN
30	33	61.1	156	1 CR18_ORYSA	Q06997 oryza sativ	CR18_ORYSA
31	33	61.1	274	1 AROE_SEEAE	P43004 pseudomas	AROE_SEEAE
32	33	61.1	295	1 ISPA_PASMU	P57133 pastuerella	ISPA_PASMU
33	61.1	1 IHA_TRIVU	077755 trichosurus	077755	077755	IHA_TRIVU

DR	PROSITE: PS0053; BETA_ELM_LYASE; 1.	RQ	aromatic amino acids in <i>Escherichia coli</i> .";
KW	tryptophan catabolism; Lyase; Pyridoxal phosphate; Complete proteome.	RL	J. Bacteriol. 173:3231-3234(1991).
FT	BINDING	RL	[7]
SEQUENCE	471 AA; 52799 MW; 49D2D41BD9D0034 CRC64;	RN	SEQUENCE OF 1-12.
Db	410 QLPCPARELLR 419	RC	STRAIN=K12 / ENZYME;
	Best Local Similarity 100.0%; Pred. No. 0.021; 0; Mismatches 0; Indels 0; Gaps 0;	RX	MEDLINE=9144395; PubMed=9298646;
RESULT 2		RA	Link A.J., Robison K., Church G.M.;
TNAA_ECOLI		RT	"Comparing the predicted and observed properties of proteins encoded
ID	TNAA_ECOLI STANDARD; PRT; 471 AA.	RL	in the genome of <i>Escherichia coli</i> K-12.";
AC	P00913; P78123; STANDARD; PRT; 471 AA.	RN	Electrophoresis 18:1259-1313(1997).
DT	21-JUL-1986 (Rel. 01, Created)	RP	[18] MUTAGENESIS OF CYS-294 AND CYS-298.
	01-JUL-1993 (Rel. 26, Last sequence update)	RX	MEDLINE=89278130; PubMed=2659590;
DT	15-JUN-2002 (Rel. 41, Last annotation update)	RA	Phillips R.S., Gollnick P.D.;
DE	TRYPTOPHANASE (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).	RT	"Evidence that cysteine 298 is in the active site of tryptophan
TNAA	OR INND OR B3708.	RL	indole-lyase.";
OS	Escherichia coli	CC	J. Biol. Chem. 264:10627-10632(1989).
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	CC	-I - CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
OX	Escherichia.	CC	NH(3).
NCBI_TaxID=562;		CC	-I - COFACTOR: Pyridoxal phosphate.
RP	SEQUENCE FROM N.A.	CC	-I - PATHWAY: Tryptophan catabolism.
RT	"Nucleotide sequence of the structural gene for tryptophanase of	CC	-I - SUBUNIT: Homotetramer.
RC	STRAIN=K12;	CC	-I - SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
RA	Deely M.C., Yanofsky C.;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RX	"Nucleotide sequence of the structural gene for tryptophanase of	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA	Escherichia coli K-12.";	CC	the European Bioinformatics Institute. There are no restrictions on its
RL	J. Bacteriol. 147:787-796(1981).	CC	use by non profit institutions as long as its content is in no way
RN	[21]	CC	modified and this statement is not removed. Usage by and for commercial
RP	SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RC	STRAIN=B1/17-A;	CC	
RX	MEDLINE=8923226; PubMed=2520187;	DR	EMBL; K00032; RAA24676; 1; -
RA	TKUDUSHIGE M., TSUJIMOTO N., ODA T., HONDA T., YUMOTO N., ITO S.,	DR	EMBL; X15974; CAM34095; 1; -
RT	YAMAMOTO M., KIM E.H., HIRAGI T.;	DR	EMBL; M11990; RAA24679; 1; -
RT	"Role of cysteine residues in tryptophanase for monovalent cation-	DR	EMBL; M59914; -; NOT_ANNOTATED_CDS.
RT	induced activation.";	DR	EMBL; L10328; AAC62059; 1; ALT_INIT.
RL	Biochimie 71:711-720(1989).	DR	EMBL; AE00148; AAC76731; 1; ALT_INIT.
RN	[3]	DR	EMBL; A01136; WZEC.
RP	SEQUENCE FROM N.A.	DR	RESP; P28796; TAX4.
RC	STRAIN=K12 / M031655;	DR	ECODATABASE; G045; 5; 6TH EDITION.
RX	MEDLINE=931513; PubMed=7686892;	DR	EcoGene; EG31005; tnba.
RA	BURLAND V.D., PUNKERT G. III, DANIELS D.L., BLATTNER F.R.;	DR	InterPro; IPR001597; Beta_elim_lyase.
RT	"DNA sequence and analysis of 136 kilobases of the <i>Escherichia coli</i>	DR	ProDom; PD005927; Beta_elim_lyase; 1.
RT	genome: organizational symmetry around the origin of replication.";	DR	PROSITE; PS00853; BETA_ELM_LYASE; 1.
RL	Genomics 16:551-561(1993).	FT	TRYPTOPHAN catabolism; Lyase; Pyridoxal phosphate; Complete proteome.
RN	[4]	FT	BINDING 270 270 PYRIDOXAL PHOSPHATE.
RP	SEQUENCE OF TRYPtic PEPTIDES.	FT	MUTAGEN 294 294 C>S: IDENTICAL TO WID-TYPE.
RC	STRAIN=K12;	FT	MUTAGEN 298 C>S: ALTERED ACTIVITY.
RX	MEDLINE=72134424; PubMed=4551944;	FT	CONFFLICT 137 140 DITG -> TTGC (IN REF. 1).
RA	KAGAMIYA H., MATSUBARA H., SNELL E.E.;	FT	CONFLICT 379 380 QA -> TG (IN REF. 1 AND 2).
RT	"The chemical structure of tryptophanase from <i>Escherichia coli</i> K-12.";	FT	SEQUENCE 471 AA; 52773 MW; 5AFC1F41BD9D0034 CRC64;
RT	operc expression in <i>Escherichia coli</i> K-12.;"	QY	1 QLPCPARELLR 10
RL	J. Bacteriol. 164:731-740(1985).	DB	410 QLPCPARELLR 419
RN	[6]		
RP	SEQUENCE OF 463-471 FROM N.A.		
RA	MEDLINE=91216998; PubMed=2026260;		
RA	SASBERO J.P., WOOKEY P.J., GOLINICK P.D., YANOFSKY C., PITTED A.J.;		
RA	"A new family of integral membrane proteins involved in transport of		
RESULT 3			
TNAA_PASMU			
ID	TNAA_PASMU STANDARD; PRT; 471 AA.		
AC	Q9C127;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DE	TRYPTOPHANASE (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).		
GN	TNAA OR P1M420		
OS	Pasteurella multocida		

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OC NCBI_TaxID=747;
 RN [1] SEQUENCE FROM N.A.;
 RC STRAIN="pm70;"
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001);
 CC -1- CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
 CC NH(3);
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Tryptophan catabolism.
 CC -1- SUBUNIT: Homotetrramer (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC DR EMBL; AF003252; AAB96579.1; -.
 CC DR FSSP; P28796; 1AX4.
 CC DR InterPro; IPR01597; Beta_elim_lyase.
 CC DR Pfam; PF01212; Beta_elim_lyase; 1.
 CC DR PROSITE; PS00853; BETA_ELM_LYASE; 1.
 CC KW TRYPTOPHAN catabolism; Lyase; Pyridoxal phosphate.
 CC FT BINDING 270
 CC SQ SEQUENCE 471 AA; 53893 MW; B6DE14FF17BF8E CRC94;
 CC
 Query Match 100.0%; Score 54; DB 1; Length 471;
 Best local Similarity 100.0%; Pred. No. 0.021; Mismatches 10; Indels 0; Gaps 0;
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 QY 1 QLCPCPAELLR 10
 Db 410 QLCPCPAELLR 419
 CC
 RESULT 4
 ID TNA_HA1N STANDARD; PRT; 472 AA.
 AC 007674;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRYPTOPHANASE (EC 4.1.99.1) (L-Tryptophan indole-lyase) (TNase).
 GN TNA OR VCA0161.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OC NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN="El Tor" NI6961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Erdmann M.D., Yamatievean J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RL Nature 406:477-483 (2000).
 RN [2]
 RP SEQUENCE OF 51-241 FROM N.A.
 RC STRAIN="Bengal".
 RA Tang T.H., Ravichandran M., Johari M.R., Zainuddin Z.F.,
 RT "Vibrio cholerae putative tryptophanase gene partial cds.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
 CC NH(3);
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Tryptophan catabolism.
 CC -1- SUBUNIT: Homotetrramer (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
 CC
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CC

DR EMBL: AE004357; AAF56074.1; .

DR HSSP: P28196; TAX4.

DR TIGR; VCA0161; .

DR InterPro; IPR001597; Beta_elim_lyase.

DR pfam; PF0121; Beta_elim_lyase; 1.

DR PRODOM; PD005927; Beta_elim_lyase; 1.

DR PROSITE; PS0053; BETA_ELIM_LYASE; 1.

KW TRYPTOPHAN catabolism; Lyase; Pyridoxal phosphate; Complete proteome.

FT BINDING 270 270 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 472 AA; 52920 MW; 632384154C06F7B9 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 472;

Best Local Similarity 90.0%; Pred No. 0.36;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QLPCPAELLR 10

Db 410 QHPCPAELLR 419

RESULT 6

ML64_HUMAN STANDARD; PRT; 445 AA.

ID ML64_HUMAN STANDARD; PRT; 445 AA.

AC 01849; 096H9; Published=7490069;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE MLN 64 Protein (CAB1 protein) (Stard3).

GN MLN64 OR CAB1 OR STARD3.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarchini; Homioidea; Homo.

NCBI-TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Breast carcinoma;

RX MEDLINE=96039245; Published=7490069;

RA Tomasetto C., Regnier C., Moog-Lutz C., Mattei M.-G., Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;

RT "Identification of four novel human genes amplified and overexpressed in breast carcinoma and localized to the q11-q21.3 region of chromosome 17.";

RT Genomics 28:367-376(1995).

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Gesophagel carcinoma;

RX MEDLINE=9713649; Published=92770027;

RA Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M., Hirai H., Yazaki Y., Sugimura T., Terada M.;

RT "Isolation of a candidate gene, CAB1, for cholesterol transport to mitochondria from the c-EGRB2 amplicon by a modified cDNA selection method";

RT Cancer Res. 57:3548-3553(1997).

RN [3] SEQUENCE FROM N.A.

RC TISSUE=Lung, Skin, and Spleen;

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RN [4] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.

RX MEDLINE=2056452; Published=10802740;

RA Tsujihita Y., Hurley J.H.;

RT "Structure and lipid transport mechanism of a STAR-related domain.";

RL Nat. Struct. Biol. 7:408-414(2000).

CC -I- FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain.

CC -I- SIMILARITY: CONTAINS 1 START DOMAIN.

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CC

DR EMBL; X80198; CAM56489.1; .

DR EMBL; D38255; BAR22528.1; .

DR EMBL; BC008256; AAH08256.1; .

DR EMBL; BC025679; AAH25679.1; .

DR EMBL; 607048; .

MIM: 607048; .

DR InterPro; IPR002013; START.

DR InterPro; IPR000799; STAR.

PRIM: PR01852; SPART; 1.

PRINTS: PRO0970; STARROTEIN.

SMART; SM00334; START; 1.

PROSITE; PS050848; START; 1.

Db 289 LPCPAELV 296

RESULT 7

ML64_MOUSE STANDARD; PRT; 446 AA.

ID ML64_MOUSE STANDARD; PRT; 446 AA.

AC 061542; Published=7490069;

DT 30-MAY-2000 (Rel. 39, Created)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE MLN 64 protein (ES 64 protein) (Stard3).

GN MLN64 OR ES64 OR STARD3.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI-TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Breast;

RX MEDLINE=9603945; Published=7490069;

RA Tomasetto C., Regnier C.H., Moog-Lutz C., Mattei M.-G., Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;

RT "Identification of four novel human genes amplified and overexpressed in breast carcinoma and localized to the q11-q21.3 region of chromosome 17.";

RT Genomics 28:367-376(1995).

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Breast;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -I- FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain (By similarity).

CC -I- SIMILARITY: CONTAINS 1 START DOMAIN.

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CC

DR InterPro; IPR002913; START.

DR InterPro; IPR000799; STAR.

DR Pfam; PF01852; START: 1.

DR PRINTS; PR00978; STARPROTEIN.

DR SMART; SM00234; START: 1.

DR PROSITE; PS50348; START: 1.

DR PROSITE; PS50234; WD_REPEATS_2; 2.

DR PROSITE; PS5024; WD_REPEATS_REGION; 1.

DR Repeat; WD repeat.

KW Repeat; WD repeat.

FT REPEAT 11 52 WD 1.

FT REPEAT 69 108 WD 2.

FT REPEAT 143 182 WD 3.

FT REPEAT 185 224 WD 4.

FT REPEAT 371 413 WD 5.

Query Match 75..9%; Score 41; DB 1; Length 468;

Best Local Similarity 87..5%; Pred. No. 4;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPPCAELL 9

Db 290 LPPCAELLV 297

RESULT 8

CAC2_YEAST STANDARD; PRT: 468 AA.

ID CAC2_YEAST STANDARD; PRT: 468 AA.

AC 004159; Rel. 35, Created 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Chromatin assembly factor 1 P60 subunit (CAF-1 60 kDa subunit).

GN CAC2 OR YML102W

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TAXID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RA Devlin K., Churcher C., Barrell B.G., Rajandream M.A.; submitted (AUG-1994) to the EMBL/genBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 5B..83 AND 459..468, AND CHARACTERIZATION.

RX MEDLINE-97182548; PubMed=9036687;

RA Kaufman R.D., Kobayashi R., Stillman B.; "Ultraviolet radiation sensitivity and reduction of telomeric silencing in *Saccharomyces cerevisiae* cells lacking chromatin assembly factor 1". *Genes Dev.* 11:345..357(1997).

CC -1- FUNCTION: COMPLEX THAT ASSEMBLES HISTONE OCTAMERS ONTO REPLICATING DNA IN VITRO. CAF-1 PERFORMS THE FIRST STEP OF THE NUCLEOSOME ASSEMBLY PROCESS, BRINGING NEWLY SYNTHESIZED HISTONES H3 AND H4 TO PREPLICATING DNA. HISTONES H2A/H2B CAN BIND TO THIS CHROMATIN PRECURSOR SUBSEQUENT TO DNA REPLICATION TO COMPLETE THE HISTONE OCTAMER. P150 AND P60 FORM COMPLEXES WITH NEWLY SYNTHESIZED HISTONES H3 AND ACETYLATED H4 IN CELL EXTRACTS (BY SIMILARITY).

CC -1- SUBUNIT: COMPOSED OF THREE SUBUNITS, P50, P60 AND P90.

CC -1- SUBCELLULAR LOCATION: nuclear.

CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).

CC -1- SIMILARITY: BELONGS TO THE HIRI FAMILY OF WD REPEAT PROTEINS.

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CC EMBL; X80835; CAA56795.1; -.

DR SGD; S0004570; CAC2.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 5.

DR PRINTS; PR00320; GPIPROTINBRPT.

DR SMART; SM00320; WD40; 5.

DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NBG.

DR PROSITE; PS50082; WD_REPEATS_2; 2.

DR PROSITE; PS5024; WD_REPEATS_REGION; 1.

DR Repeat; WD repeat.

KW Repeat; WD repeat.

FT REPEAT 11 52 WD 1.

FT REPEAT 69 108 WD 2.

FT REPEAT 143 182 WD 3.

FT REPEAT 185 224 WD 4.

FT REPEAT 371 413 WD 5.

Query Match 75..9%; Score 41; DB 1; Length 468;

Best Local Similarity 60..0%; Pred. No. 4..2;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QLPPCAELLR 10

Db 237 ELPCPGDVLK 246

RESULT 9

RNH2_XYLFA STANDARD; PRT: 234 AA.

ID RNH2_XYLFA STANDARD; PRT: 234 AA.

AC 09PE17; Rel. 40, Created 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ribonuclease HII (EC 3.1.26.4) (RNase HII).

GN RNHB OR XR1041.

OS *Xylella fastidiosa*.

OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; *Xylella*.

OX NCBI_TAXID=2371;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=985C;

RA MEDLINE-20365171; PubMed=10910347;

RA Simpson A.J., Reinach F.C., Arruda P., Abreu F.A., Aencencio M., Alvarez R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barrros M.H., Bonaccorsi E.D., Bordim S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrero D.M., Carreiro H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto E., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Borry H., Facincani A., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furian L.R., Garnier M., Goldman G.H., Goldinan M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Taiget F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhai A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santalli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., dasilva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsinako M.H., Valleda H., Van Sluys M.A., Verjoshi-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen *Xylella fastidiosa*."; Nature 405:151-159(2000).

CC -1- FUNCTION: THIS ENZYME IS AN ENDONUCLEASE THAT DEGRADES THE RNA OF RNA-DNA HYBRIDS SPECIFICALLY (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphomonoester.

DR EMBL; M85197; AAA21159.1; - .

DR PIR; C43384; C43584.

DR InterPro; IPR03506; Chlam_OMP6.

DR Pfam; PF03504; Chlam_OMP6; 1.

DR PRINTS; PR01336; CHLAMIDIOM6.

KW Outer membrane; Transmembrane; Signal; Virulence.

FT SIGNAL 1 22

FT PROPER 23 40

FT CHAIN 41 547 AA; 58694 MW; 60 kDa OUTER MEMBRANE PROTEIN, SEROVAR C.

SQ SEQUENCE 547 AA; 139 QLPCEAEFVR 148

Query Match 72.2%; Score 39; DB 1; Length 547;

Best Local Similarity 70.0%; Pred No. 11; Mismatches 1; Conservative 1; Indels 2; Gaps 0; Gaps 0;

Qy 1 QLPCEAEFVR 10

Db 139 QLPCEAEFVR 148

RESULT 12

OM6D_CHLTR

ID OM6D_CHLTR STANDARD; PRT; 547 AA.

AC P18151;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 60 kDa outer membrane protein precursor (Cysteine-rich outer membrane protein) (CRP) (60 kDa cysteine-rich OMP).

DE protein OR CRP) (60 kDa cysteine-rich OMP).

GN OMCP2 OR OM2B OR CT443.

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

[1]

RP SEQUENCE FROM N.A.

RX STRAIN=B/TW-5/OT;

RX MEDLINE=90128208; PubMed=2612891;

RA Watson M.W., Lambdin P.R., Ward M.E., Clarke I.N.;

RT "Chlamydia trachomatis 60 kDa cysteine rich outer membrane protein: sequence homology between trachoma and lgv biologics.";

RT FEMS Microbiol. Lett. 53:293-297(1989).

[2]

RN RP SEQUENCE FROM N.A.

RX STRAIN=B/TW-5/OT;

RX MEDLINE=91141306; PubMed=2287277;

RA Allen J.E., Cerrone M.C., Beatty P.R., Stephens R.S.;

RT "Cysteine-rich outer membrane proteins of Chlamydia trachomatis display compensatory sequence changes between biovariants.";

RT Mol. Microbiol. 4:1543-1550(1990).

[3]

RN RP SEQUENCE FROM N.A.

RX STRAIN=D/W-3/CX;

RX MEDLINE=99000809; PubMed=974136;

RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;

RA "Genome sequence of an obligate intracellular pathogen of humans:

RT Chlamydia trachomatis.";

RL Science 282:754-759(1998).

CC -1- FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES (RBS) INTO ELEMENTARY BODIES (EBS). IT IS NECESSARY FOR STRUCTURAL INTEGRITY OF THE EBS OUTER ENVELOPE. IT MAY ALSO BE AN IMPORTANT VIRULENCE FACTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

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CC

DR EMBL; X55110; CAA37588.1; - .

DR PIR; AE00131; AAC68042.1; ALT_INIT.

DR InterPro; IPR03506; Chlam_OMP6.

DR Pfam; PF03504; Chlam_OMP6; 1.

DR PRINTS; PR01336; CHLAMIDIOM6.

KW Outer membrane; Transmembrane; Signal; Virulence; Complete proteome.

FT SIGNAL 1 22

FT PROPER 23 40

FT CHAIN 41 547 AA; 58694 MW; 60 kDa OUTER MEMBRANE PROTEIN.

SQ SEQUENCE 547 AA; 139 QLPCEAEFVR 148

Query Match 72.2%; Score 39; DB 1; Length 547;

Best Local Similarity 70.0%; Pred No. 11; Mismatches 1; Conservative 1; Indels 2; Gaps 0; Gaps 0;

Qy 1 QLPCEAEFVR 10

Db 139 QLPCEAEFVR 148

RESULT 13

OM6E_CHLTR

ID OM6E_CHLTR STANDARD; PRT; 547 AA.

AC P23603;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 60 kDa outer membrane protein, serovar B precursor (Cysteine-rich outer membrane protein) (60-kDa CRP).

DE OMCP2 OR OM2B.

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=DK 20

RX MEDLINE=9106746; PubMed=2251143;

RA Coles A.M., Allan I., Pearce J.H.;

RT "The nucleotide and derived amino acid sequence of the omp2 gene of Chlamydia trachomatis serovar E.";

RA Nucleic Acids Res. 18:6713-6713(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=BOUR / Serovar E;

RX MEDLINE=91147205; PubMed=1997423;

RA de la Maza L.M., Fiedler T.J., Carlson E.J., Markoff B.A., Peterson E.M.;

RT Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton protein between the trachoma and lymphogranuloma venereum biovars of Chlamydia trachomatis.";

RT Infect. Immun. 59:1196-1201(1991).

RN [3]

RP SEQUENCE FROM N.A.

RA Zhang Y.X., Caldwell H.D.;

RT Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.

CC -1- FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES (RBS) INTO ELEMENTARY BODIES (EBS). IT IS NECESSARY FOR STRUCTURAL INTEGRITY OF THE EBS OUTER ENVELOPE. IT MAY ALSO BE AN IMPORTANT VIRULENCE FACTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN DK 20.

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CC

DR EMBL; X55903; CAA39395.1; -.
 DR EMBL; X54389; CAA38225.1; -.
 DR EMBL; M65196; AAA22154.1; -.
 DR PIR; S13120; S13120.
 DR InterPro; IPR003506; ChlamOMP6.
 DR Pfam; PF0304; ChlamOMP6_1.
 DR PRINTS; PRO1336; CHLAMIDIOM6.
 KW Outer membrane; Transmembrane; Signal; Virulence.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 40
 FT CHAIN 41 547 60 kDa OUTER MEMBRANE PROTEIN, SEROVAR E.
 FT VARIANT 33 34 SL -> FT (IN STRAIN DK20).
 FT VARIANT 121 121 I -> L (IN STRAIN DK20).
 FT VARIANT 132 132 V -> A (IN STRAIN DK20).
 FT VARIANT 132 132 N -> S (IN STRAIN DK20).
 SO SEQUENCE 547 AA; 58708 MW; 052066084#E20AB CRG64;
 DR PRINTS; PRO1336; CHLAMIDIOM6.
 DR Best Local Similarity 70.0%; Pred. No. 11; Length 547;
 DR Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 DR QY 1 QLPCPAELLR 10
 DR Db 139 QLPCCEAEFVR 148

RESULT 14

ID OM6LCHTR	STANDARD;	PRT; 547 AA.
AC P21354;		
DT 01-NOV-1990 (Rel. 16, Created)		
RP 01-MAY-1991 (Rel. 18, Last sequence update)		
DT 15-JUN-2002 (Rel. 41, Last annotation update)		
DE 60 kDa outer membrane protein, serovars L1/L2/L3 precursor (Cysteine-rich outer membrane protein (60-kDa CRP)).		
GN Omp2 or OMP2B.		
OS Chlamydia trachomatis.		
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
OX NCBI_TAXID=813;		
RN [1]		
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC STRAIN=L2/434/Bu;		
RX MEDLINE=69123030; PubMed=2314847;		
RA Allen J.E., Stephens R.S.;		
RT "Identification by sequence analysis of two-site posttranslational processing of the cysteine-rich outer membrane protein 2 of Chlamydia trachomatis serovar L2";		
RT J. Bacteriol. 171:285-291(1989).		
RL [2]		
RN SBQUENCE FROM N.A.		
RC STRAIN=L2/434/Bu;		
RX MEDLINE=9147205; PubMed=1997423;		
RA de la Maza L.M., Fiedler T.J., Carlson E.J., Markoff B.A.,		
RA Peterson E.M.;		
RT "Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton protein between the trachoma and lymphogranuloma venereum biovars of Chlamydia trachomatis.;"		
RL Infect. Immun. 59:1196-1201(1991).		
RN [3]		
RP SEQUENCE FROM N.A.		
RC STRAIN=L440/LN;		
RX MEDLINE=89138006; PubMed=3066701;		
RA Clarke I.N., Ward M.E., Lambden P.R.;		
RT "Molecular cloning and sequence analysis of a developmentally regulated cysteine-rich outer membrane protein from Chlamydia trachomatis." Gene 71;307-314(1988).		
RL Gene 71;307-314(1988).		
CC FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES (RBs) INTO ELEMENTARY BODIES (EBs). IT IS NECESSARY FOR STRUCTURAL INTEGRITY OF THE EBs OUTER ENVELOPE. IT MAY ALSO BE AN IMPORTANT VIRULENCE FACTOR.		
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.		

Query Match 72.2%; Score 39; DB 1; Length 547;
 Best Local Similarity 70.0%; Pred. No. 11; Length 547;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QLPCPAELLR 10
 DR Db 139 QLPCCEAEFVR 148

RESULT 15

ID SRC_CLOBE	STANDARD;	PRT; 632 AA.
AC P26047; Q9LX1;		
DT 01-MAY-1992 (Rel. 22, Created)		
RP 16-OCT-2001 (Rel. 40, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Signal-transduction and transcriptional-control protein.		
GN SRC.		
OS Clostridium beijerinckii (Clostridium MP)		
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium;		
OX NCBI_TAXID=1520;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=NRRL B593;		
RA Rifaat M.M., Chen J.S.;		
RT "The predicted protein product of a putative regulatory gene from Clostridium beijerinckii NRRL B593 is homologous to the NtrC subfamily of transcriptional regulators.;"		
RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.		
CC -1- SIMILARITY: THE N-TERMINAL REGION CONTAINS A SIGMA-54 FACTOR		
CC INTERACTION: ATP-BINDING DOMAIN.		
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.		
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CC DR EMBL; AF157307; AAD54950.1; -.		
CC DR InterPro; IPR003593; AAA_APase. -		
CC DR InterPro; IPR02197; HTH_FIS.		
CC DR InterPro; IPR00014; PAS_domain.		
CC DR InterPro; IPR02078; Sig54_Interact.		

DR Pfam; PF00158; SIGMA54_ACTIVAT; 1.
DR Pfam; PF00989; PAS; 1.
DR Pfam; PF02954; HTH_B; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00091; PAS; 1.
DR TIGRFAMS; TIGR00229; sensory_box; 1.
DR TIGRFAMS; TIGR01199; HTH_fis; 1.
DR PROSITE; PS50112; PAS; 1.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
DR PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
DR PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
DR PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
KW Transcription regulation; Sensory transduction; DNA-binding;
KW ATP-binding. 197 270
FT DOMAIN 324 554
FT NP_BIND 352 359
FT NP_BIND 416 425
FT DNA_BIND 606 625
SQ SEQUENCE 632 AA; 71537 MW; C52A3D906BB0B2CA CRC64;

Query Match 70.4%; Score 38; DB 1; Length 632;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LPCPAELLR 10
Db 27 IPCPSKLLR 35

Search completed: July 9, 2003, 12:00:43
Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:57:21 ; Search time 35.5 seconds
 {without alignments)
 58.041 Million cell updates/sec

Title: US-09-851-058-1
 Perfect score: 54
 Sequence: 1 QMPCPAPELLR 10

Scoring table: BLOSSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTRIMBL_21:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rhodent:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriaph:
 17: sp_archeap:
 18: sp_bacteriophage:
 19: sp_chlorophyta:
 20: sp_ciliates:
 21: sp_eukaryota:
 22: sp_hexameric:
 23: sp_hexameric:
 24: sp_hexameric:
 25: sp_hexameric:
 26: sp_hexameric:
 27: sp_hexameric:
 28: sp_hexameric:
 29: sp_hexameric:
 30: sp_hexameric:
 31: sp_hexameric:
 32: sp_hexameric:
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 40: sp_hexameric:
 41: sp_hexameric:
 42: sp_hexameric:
 43: sp_hexameric:
 44: sp_hexameric:
 45: sp_hexameric:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	40	74	1	Q961H8 homo sapien
2	40	74	1	Q9MAA9 arabidopsis
3	40	74	1	Q91179 pseudomonas
4	39	72	2	Q93FV8 chlamydia t
5	39	72	2	Q93317 chlamydia t
6	38	70	4	Q9LEB7 petroselinum
7	38	70	4	Q9PTZ3 chlamydia m
8	38	70	4	Q9A3L2 caulobacter
9	38	70	4	Q9W6I2 pimephales
10	38	70	4	Q9Y4B5 homo sapien
11	38	70	4	Q90YN8 brachydontio
12	37	68	16	Q916P4 pseudomonas
13	37	68	5	Q94W74 scarlettaeos
14	37	68	5	Q9NFC7 drosophila
15	37	68	4	Q94909 homo sapien
16	36	66	7	Q9HP51 halobacteri

ALIGMENTS

RESULT 1	ID	PRELIMINARY;	PRT;	57 AA.
0961H8	Q961H8;			
AC	Q961H8;			
DT	01-DEC-2001 (TREMBBLEL_19, Created)			
DT	01-DEC-2001 (TREMBBLEL_19, Last sequence update)			
DT	01-DEC-2001 (TREMBBLEL_19, Last annotation update)			
DE	Similar to erythroid differentiation and denucleation factor			
DE	1. Homo sapiens (Human);			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SKIN;			
RA	Strausberg R.;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC007528; AAH07528.1; -			
SQ	SEQUENCE 57 AA: 6004 MW: 2132EA21A4311176 CRC64;			

RESULT 2

Q	2	LPCPPELLR 10	
Q	2	LPCPPELLR 10	
Db	26	LPCPGDLR 34	

Query Match Best local similarity Matches; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Q9MAA9 PRELIMINARY; PRT; 336 AA.

AC Q9MAA9;

DT 01-OCT-2000 (TREMBBLEL_15, created)

DT 01-OCT-2000 (TREMBBLEL_15, last sequence update)

DT 01-JUN-2002 (TREMBBLEL_21, last annotation update)

DE T12H1.6 protein (Hypothetical 37.7 kDa protein).

GN T12H1.6 OR ATG05100.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC euroids IT; Brassicales; Brassicaceae; Arabidopsis.
 OX NEBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Niemann W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EBO04667; AAC05790.1; -.
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Goldsmith A.D., Banh J., Chang C.H., Chang E., Dale J.M.,
 RA Yamamura Y., Yu G., Yu S., Boeser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Lam J., Lam B., Lin J., Meyer M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shinji P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RT "Full length cDNA of gene At3g05100 (GT:15229893);"
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Ouach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Boeser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinji P., Southwick A., Shinozaki K.,
 RT "Arabidopsis Open Reading Frame (ORF) Clones.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AC009177; ARF27016.1; -.
 DR EMBL: AK070370; AA149868.1; -.
 DR EMBL: AV091328; AMI14267.1; -.
 DR InterPro: IPR00051; SAM_bind.
 KW Hypothetical protein.
 SO SEQUENCE 336 AA; 37719 MW; 6FA910F7B4B2FA85 CRC64;

Query Match	74.1%	Score	40	DB	15	Length	5149
Best Local Similarity	70.0%	Pred.	No. 1.4e+02				
Matches	7	Conservative	2	Mismatches	1	Indels	0
				Gaps	0		

Qy 2 LPPCAELL 9
 Db 137 LPPCAELL 144

RESULT 3

091179 PRELIMINARY; PRT; 5149 AA.
 AC 091179; PRELIMINARY;
 DT 01-MAR-2001 (TREMBREL_16, Created)
 DT 01-MAR-2001 (TREMBREL_16, Last sequence update)
 DE Probable non-ribosomal peptide synthetase.
 GN P2402.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas; NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ARCC 15692 / PA01;
 RA MEDLINE=20137337; PubMed=10984043;
 RA Stover C.K., Pham X.Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Rufnique W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goitry L., Tolentino E., Westbroek-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.;"
 RL Nature 405:959-964(2000).
 DR EBO04667; AAC05790.1; -.
 DR HSSP; P14687; IAMU
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR01242; Condensatn.
 DR InterPro; IPR00577; FGK_kin.
 DR InterPro; IPR03880; Phantme.attach.
 DR Pfam; PF00501; AMP-binding; 4.
 DR Pfam; PF00668; Condensation; 6.
 DR Pfam; PF00550; PP-binding; 4.
 DR PROSITE; PS50075; ACP DOMAIN; 4.
 DR PROSITE; PS00455; AMP BINDING; 4.
 DR PROSITE; PS00452; FGGI_KINASES_2; UNKNOWN_1.
 DR PROSITE; PS00012; PHOSPHOPANTETHINE; UNKNOWN_3.
 KW SEQUENCE 5149 AA; 569179 MW; 20575B7618921CA0 CRC64;

Query Match	74.1%	Score	40	DB	15	Length	5149
Best Local Similarity	70.0%	Pred.	No. 1.4e+02				
Matches	7	Conservative	2	Mismatches	1	Indels	0
				Gaps	0		

Qy 1 QLPCEAELLR 10
 Db 139 QLPCEAELLR 148

RESULT 5

093317 PRELIMINARY; PRT; 547 AA.
 ID 093317; PRELIMINARY;
 AC 093317; PRELIMINARY;
 DT 01-DEC-2001 (TREMBREL_19, Created)

DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	RESULT 7
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	Q9PZ3
DE	Major outer membrane protein.	PRELIMINARY;
GN	OMPA.	PRT; 265 AA.
OS	Chlamydia trachomatis.	ID Q9PZ3
OC	Bacteria; Chlamydiales; Chlamydaceae; Chlamydia.	AC Q9PZ3;
OX	NCBI_TAXID=813;	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RN	[1]	DT 01-OCT-2000 (TREMBLrel. 21, Last annotation update)
RP	SEQUENCE FROM N.A.	DE Spoo RNA methylase family protein.
RC	STRAIN=UW-12, AND UW-36;	GN TC0683.
RX	MEDLINE=21450526; PubMed=11567000;	OS Chlamydia muridarum.
RA	MILLINNE K.L., Tavares S., Dean D.;	OC Bacteria; Chlamydiales; Chlamydaceae; Chlamydia.
RT	*Recombination in the ompA Gene but Not the omcB Gene of Chlamydia	OX NCBI_TAXID=83560;
RT	Contributes to Serovar-Specific Differences in Tissue Tropism, Immune	RN [1]
RT	Surveillance, and Persistence of the Organism.";	RP SEQUENCE FROM N.A.
RL	J. Bacteriol. 183:5997-6008(2001).	RC STRAIN=MOPN / NIGG;
DR	EMBL; AF304330; ALA14100_1; -;	RX MEDLINE=20150555; PubMed=10684935;
DR	INTERPRO; IPR003506; Chlam_OMP6.	RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Linthicum K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.,
DR	PFAM; PF03504; Chlam_OMP6; 1.	RA "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39";
DR	PRINTS; PRO1316; CHLAMITIAOM6.	RT Nucleic Acids Res. 28:1397-1406(2000).
SQ	SEQUENCE 547 AA; 58626 MW; 817BA3000FEA6A71 CRC64;	EMBL; AE002337; RAE73591_1; -;
Query Match	72.2%; Score 39; DB 2; Length 547;	TIGR; TC0683;
Best Local Similarity	70.0%; Pred. No. 28;	DR Interpro; IPR001537; Spoo_methylase.
Matches	7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	DR Pfam; PF00588; Spoo_methylase; 1.
Qy	1 QLPCPARELLR 10	DR ProDom; PD001443; Spoo_methylase; 1.
Db	139 QLPCEAEPFVR 148	DR Complete proteome; 29855 AA; F5DBB8F5A3932915 CRC64;
RESULT 6		KW SQ
Q9LEB7	PRELIMINARY;	Q9A3L2
ID	PRT; 147 AA.	ID Q9A3L2
AC	Q9LEB7;	AC Q9A3L2;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	DE Sensory box histidine kinase/response regulator.
DE	Common plant regulatory factor 6.	GN CC3191.
GN	CPRF6.	OS Caulobacter crescentus.
OS	Petroselinum crispum (Parsley) (Petroselinum hortense).	OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC Caulobacter;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	OX NCBI_TAXID=155892;
OC	Asteridae; eustephids II; Apiales; Apiaceae; Petroselinum.	RN [1]
RN	[1]	RP SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RC STRAIN=CV_HAMBURGER SCHMITT;
RC	STRAIN=CV_HAMBURGER SCHMITT; PubMed=11523788; MEDLINE=21414626; RUEGGER A., Frohmeier H., Naeye C., Wellmer F., Kircher S., Schaefer E., Harter K.;	RX MEDLINE=21173638; PubMed=11259647;
RC	"Isolation and characterization of four novel novel parsley proteins that interact with the transcriptional regulators CPRF1 and CPRF2.";	RA Eisen J., Heidelberg J.F., Alley M.R.K., Ochiai N., Madock J.R., Nelson K.E., Potocka I., Neilson W.C., Newton A., Stephens C., Phadie N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Yamatevan J.J., Emolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RC	Mol. Genet. Genomics 265:964-976(2001).	RN "Complete genome sequence of Caulobacter crescentus.";
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	RL Proc. Natl. Acad. Sci. U.S.A. 98:1316-141(2001).
CC	-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.	CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
DR	EMBL; AJ292744; CAC00657_1; -;	CC -!- REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
DR	InterPro; IPR004827; TF_BZP.	DR HSSP; P06657; 2CHF.
DR	InterPro; IPR004827; TF_BZP.	
DR	SMART; SM00338; BZP_BASIC; 1.	
DR	PROSITE; PS00036; BZP_BASIC; 1.	
DR	DNA-binding; Nuclear protein.	
DR	SEQUENCE 147 AA; 16719 MW; F03C83A5108C468D CRC64;	
Query Match	70.4%; Score 38; DB 10; Length 147;	
Best Local Similarity	85.7%; Pred. No. 13; Mismatches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Matches	1 QLPCPAB 7	
Qy	130 QLPCPAQ 136	
Db		

DR	TIGR; CC3191; -	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DR	InterPro; IPR001594; ATPbind_ANPase.	DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DR	InterPro; IPR004358; Bact_sens_pr_C.	DE	KIAA0802 protein (Fragment).
DR	InterPro; IPR003661; HIS_KinA.	GN	KIAA0802.
DR	InterPro; IPR004359; HIS_KIN_sg.	OS	Homo sapiens (Human).
DR	InterPro; IPR001610; PAC.	OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	InterPro; IPR00001; PAS_domain.	OC	Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
DR	InterPro; IPR001789; Response_reg.	NCBI_TaxID	9606;
DR	Pfam; PF00318; HATPase_c; 1.	RN	[1]
DR	Pfam; PF00072; response_reg; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00312; signal; 1.	RC	TISSUE-BRAIN;
DR	PRINTS; PRO0344; BCTRULENSOR.	RX	MEDLINE=99087487; PubMed=9872452;
DR	PRODOM; PD000039; Response_reg; 1.	RA	Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,
DR	SMART; SM00387; HATPase_c; 1.	RA	Kotani H., Nomura N., Ohara O.,
DR	SMART; SM00388; HISKA; 1.	"prediction of the coding sequences of unidentified human genes. XI.	
DR	SMART; SM00086; PAC; 2.	RT	The complete sequences of 100 new cDNA clones from brain which code
DR	SMART; SM00091; PAS; 1.	RT	for large proteins in vitro.";
DR	SMART; SM00448; REC; 1.	RL	DNA RES; 5,277-286(1998).
DR	TIGRFAMS; TIGR00229; sensory_box; 1.	DR	EMBL; AB018345; BAA34522.; -.
KW	Kinase; Phosphorylation; Sensory transduction; Transferase;	FT	NON_TER 1
KW	Complete proteolytic.	SQ	SEQUENCE 1353 AA; 150386 MW; 27A38F75B6EBD03F CRC64;
Query Match	70.4%; Score 38; DB 16; Length 642;	Query Match	70.4%; Score 38; DB 4; Length 1353;
Best Local Similarity	100.0%; Pred. No. 49;	Best Local Similarity	75.0%; Pred. No. 99;
Matches	0; Mismatches 0; Indels 0; Gaps 0;	Matches	1; Mismatches 1; Indels 0; Gaps 0;
Oy	4 CPAELLR 10	Oy	3 PCPAELLR 10
Db	340 CPAELLR 346	Db	247 PCPTELLK 254
RESULT 9	09W6I2	RESULT 11	09Y0YNB
ID	09W6I2	ID	09Y0YNB
AC	09W6I2;	AC	09Y0YNB;
DT	01-NOV-1999 (TREMBLrel. 12, Created)	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	DE	Vitellogenin_1.
DE	Vitellogenin.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OS	pimephales_promelas.	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	OC	Cyprinidae; Danio.
OC	Cyprinidae; Pimephales.	OX	NCBI_TaxID=90988;
OX	NCBI_TaxID=90988;	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE-LIVER;	RC	TISSUE-LIVER;
RA	Korte J.J., Kahl M.D., Jensen K.M., Pasha M.S., Parks L.G.,	RA	Willimski D., Voelkl A., Braunbeck T.;
RA	Leblanc G.A., Ankley G.T.;	RA	Islimer M., Willimski D., Voelkl A., Braunbeck T.;
RT	*Fathead Minnow Vitellogenin: Complementary DNA Sequence and Messenger	RT	"Gene expression of estrogen-regulated genes associated with
RT	RNA and Protein Expression after 17beta-Estradiol Treatment.;"	RT	reproduction after exposure to 17alpha-ethynodiol in zebrafish
RT	Environ. Toxicol. Chem. 19:972-981(2000).	RT	(Danio rerio).";
RL	EMBL; AF130354; AAC23878.1; -.	RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	InterPro; IPR001747; Lipid_transprt_N.	DR	EMBL; AF406784; AAC9445.1; -.
DR	InterPro; IPR001747; Lipid_transprt_N.	DR	InterPro; IPR001747; Lipid_transprt_N.
DR	Pfam; PF01347; Vitellogenin_N; 1.	DR	Pfam; PF01347; Vitellogenin_N; 1.
SEQUENCE	1339 AA; 146274 MW; C5DDF4EC4C3B1A2A CRC64;	SEQUENCE	1362 AA; 149547 MW; 35F8037F58F10BDA CRC64;
Query Match	70.4%; Score 38; DB 13; Length 1339;	Query Match	70.4%; Score 38; DB 13; Length 1362;
Best Local Similarity	100.0%; Pred. No. 98;	Best Local Similarity	100.0%; Pred. No. 99;
Matches	0; Mismatches 0; Indels 0; Gaps 0;	Matches	0; Mismatches 0; Indels 0; Gaps 0;
Oy	4 CPAELLR 10	Oy	4 CPAELLR 10
Db	453 CPAELLR 459	Db	453 CPAELLR 459
RESULT 12	0916P4	RESULT 13	0916P4
ID	0916P4	ID	0916P4
AC	0916P4;	AC	0916P4;
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Hypothetical protein PA0244.	DE	
RESULT 10	09Y4B5	PRELIMINARY;	PRT;
ID	09Y4B5	PRT;	1353 AA.
AC	09Y4B5;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		

OS	PNA244.	09NFC7	PRELIMINARY;	PRT;	405 AA.
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
OX	Pseudomonas;				
RN	NCBI_TAXID=287;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 15692 / PAO1; Published=2003;				
RX	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,				
RA	Hickey M.J., Brinkman F.S.L., Hutmacher W.O., Kovalek D.J., Lagrou M.,				
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,				
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA	Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;				
RT	*complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen.;				
RL	Nature 406:959-964 (2000).				
DR	EMBL: AE04462; AAC03633.1; -				
DR	InterPro: IPR00205; NAD-binding.				
DR	InterPro: IPR00207; Shikimate_DH.				
DR	InterPro: IPR00594; Thif_domain.				
DR	PF01488; Shikimate_DH; 1.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 284 AA; 29691 MW; 1B5CFF77FC/F473A CRC64;				
Query Match	Score 68.5%; Score 37; DB 16; Length 284;				
Best Local Similarity	77.8%; Pred No. 36; Mismatches 1; Indels 0; Gaps 0;				
Matches	7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
Qy	2 LPPCAPELLR 10				
Db	211 MPVPAELLR 219				
RESULT 13					
094W74	PRELIMINARY;	PRT;	348 AA.		
ID	094W74				
AC	094W74;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	NADH dehydrogenase subunit 2.				
OS	Scartella histophorus (walking goby).				
OG	Mitochondrion.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Perciformes; Gobioidae;				
OC	Gobiidae; Scartellidae.				
OX	NCBI_TaxID=156764;				
RN	[1] J. Molecular phylogeny of the Gobiodid Fishes.;				
RP	SEQUENCE FROM N.A.				
RC	TRACKER_C.E.; STRAIN=SCAHT;				
RQ	RT				
RL	*Molecular phylogeny of the Gobiodid Fishes.;				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+)+ UBIQUINOL.				
DR	EMBL: AF391490; AAL16501.1; -				
DR	InterPro: IPR001750; oxidored_q1.				
DR	PFam: PF00361; oxidored_q1; 1.				
KW	Mitochondrion; NADH Oxidoreductase; Ubiquinone.				
SQ	SEQUENCE 348 AA; 37552 MW; BB0272103A688FC3 CRC64;				
Query Match	Score 68.5%; Score 37; DB 8; Length 348;				
Best Local Similarity	65.7%; Pred No. 43; Mismatches 1; Indels 0; Gaps 0;				
Matches	6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
Qy	1 QLPCPAELL 9				
Db	144 QLPCPFSQKL 152				
RESULT 15					
OY	2 LPPCAPELL 9				
Db	405 AA; 45063 MW; DCCAO90527469769B CRC64;				
SQ	SEQUENCE 405 AA; CG18843;				
Query Match	Score 68.5%; Score 37; DB 5; Length 405;				
Best Local Similarity	75.0%; Pred No. 50; Mismatches 1; Indels 0; Gaps 0;				
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
Qy	2 LPPCAPELL 9				
Db	140 LPCCPV DLL 147				
RESULT 14					

DT 01-MAY-1999 (TREMBrel). 10, Last sequence update)
DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
DE KIAA0819 protein (Fragment).
GN KIAA0819.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes
RT XII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL: AB020265; BAA74842.1; -
DR InterPro: IPR002865; PRCHEXTENSN.
DR PRINTS: PR01217; PRCHEXTENSN.
FT NON-TER 1
SQ SEQUENCE 989 AA; 109888 MW; F8845C9CB90D7671 CRC64;
Query Match 68.5%; Score 37; DB 4; Length 989;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLPCPAE 7
Db 105 RLPCPAE 111
Search completed: July 9, 2003, 12:02:01
Job time : 38.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:55:35 ; Search time 22 Seconds
(without alignments)

30.284 Million cell updates/sec

Title: US-09-851-058-2
Perfect score: 30
Sequence: 1 YSOCR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	100.0	87 22	AAG08211 Human polypeptide
2	30	100.0	243 21	AAY28425 Rice branched chain
3	27	90.0	39 21	AKD12153 Arabidopsis thaliana
4	27	90.0	52 22	AAG77659 Human colon cancer
5	27	90.0	92 22	ABG16655 Novel human diaigo
6	27	90.0	124 21	AB445287 Human ORF146 prote
7	27	90.0	124 23	ABP31173 Rat eosinophil cat
8	27	90.0	134 23	AAW59178 Novel human diaigo
9	27	90.0	153 22	ABG09610 Rat eosinophil cat
10	27	90.0	155 19	AAW59177

ALIGNMENTS

11	27	90.0	155 20	AAW94272 Rat-derived eosino
12	27	90.0	155 20	AAW94273 Novel eosinophils-de
13	27	90.0	187 22	ABG13128 Drosophila melanog.
14	27	90.0	320 22	ABB59567 Arabidopsis thalia
15	27	90.0	424 21	ABB59585 Drosophila melanog.
16	27	90.0	585 22	BAL65855 Drosophila melanog.
17	27	90.0	755 22	ABB58301 HEV strain protein
18	27	90.0	1693 12	AAR16118 Hepatitis E virus
19	27	90.0	1693 15	AAR51264 Hepatitis E virus
20	27	90.0	1693 17	AAR9813 Hepatitis E virus
21	27	90.0	1693 19	AAW81519 Hepatitis E virus
22	27	90.0	1693 19	AAW80196 Protein encoded by Hepatitis E virus
23	27	90.0	1693 19	AAW76368 HEV-US1 ORF1 prote
24	27	90.0	1693 19	AAW71209 Swine HEV ORF 1 pr
25	27	90.0	1693 21	AHG09042 Novel human diagno
26	27	90.0	1693 22	AKR15252 Antileukoprotease
27	27	90.0	1698 20	AYA31381 Carbhydrate bindi
28	27	90.0	1707 22	ABG73750 Mutein #1 of secre
29	27	90.0	1708 20	AYA31384 Mutein #1 of secre
30	27	90.0	1708 20	AAW94408 Antileukoprotease
31	27	90.0	2228 22	AAW01844 Novel human diagno
32	26	86.7	32 12	AKY2451 Antileukoprotease
33	26	86.7	46 17	AAW00558 Human neuroendocr
34	26	86.7	51 17	ABG21573 Novel human diagno
35	26	86.7	53 18	AAW06556 Propionibacterium
36	26	86.7	58 18	AAW01845 Propionibacterium
37	26	86.7	58 18	AAW01844 Propionibacterium
38	26	86.7	61 19	AAW24451 Propionibacterium
39	26	86.7	63 22	ABG21502 Mutain #1 of secre
40	26	86.7	69 22	AAU45102 Mutain #1 of secre
41	26	86.7	71 22	AAU44863 Antileukoprotease
42	26	86.7	75 22	AAU54472 Antileukoprotease
43	26	86.7	78 22	AAU62439 Antileukoprotease
44	26	86.7	98 17	AAW00663 Human neuroendocr
45	26	86.7	103 22	ABH44333 Novel human diagno
46	26	86.7	103 22	AAU44863 Antileukoprotease
47	26	86.7	103 22	AAU54472 Antileukoprotease
48	26	86.7	103 22	AAU62439 Antileukoprotease
49	26	86.7	103 22	AAU44863 Antileukoprotease
50	26	86.7	103 22	AAU54472 Antileukoprotease
51	26	86.7	103 22	AAU62439 Antileukoprotease
52	26	86.7	103 22	AAU44863 Antileukoprotease
53	26	86.7	103 22	AAU54472 Antileukoprotease
54	26	86.7	103 22	AAU62439 Antileukoprotease
55	26	86.7	103 22	AAU44863 Antileukoprotease
56	26	86.7	103 22	AAU54472 Antileukoprotease
57	26	86.7	103 22	AAU62439 Antileukoprotease
58	26	86.7	103 22	AAU44863 Antileukoprotease
59	26	86.7	103 22	AAU54472 Antileukoprotease
60	26	86.7	103 22	AAU62439 Antileukoprotease
61	26	86.7	103 22	AAU44863 Antileukoprotease
62	26	86.7	103 22	AAU54472 Antileukoprotease
63	26	86.7	103 22	AAU62439 Antileukoprotease
64	26	86.7	103 22	AAU44863 Antileukoprotease
65	26	86.7	103 22	AAU54472 Antileukoprotease
66	26	86.7	103 22	AAU62439 Antileukoprotease
67	26	86.7	103 22	AAU44863 Antileukoprotease
68	26	86.7	103 22	AAU54472 Antileukoprotease
69	26	86.7	103 22	AAU62439 Antileukoprotease
70	26	86.7	103 22	AAU44863 Antileukoprotease
71	26	86.7	103 22	AAU54472 Antileukoprotease
72	26	86.7	103 22	AAU62439 Antileukoprotease
73	26	86.7	103 22	AAU44863 Antileukoprotease
74	26	86.7	103 22	AAU54472 Antileukoprotease
75	26	86.7	103 22	AAU62439 Antileukoprotease
76	26	86.7	103 22	AAU44863 Antileukoprotease
77	26	86.7	103 22	AAU54472 Antileukoprotease
78	26	86.7	103 22	AAU62439 Antileukoprotease
79	26	86.7	103 22	AAU44863 Antileukoprotease
80	26	86.7	103 22	AAU54472 Antileukoprotease
81	26	86.7	103 22	AAU62439 Antileukoprotease
82	26	86.7	103 22	AAU44863 Antileukoprotease
83	26	86.7	103 22	AAU54472 Antileukoprotease
84	26	86.7	103 22	AAU62439 Antileukoprotease
85	26	86.7	103 22	AAU44863 Antileukoprotease
86	26	86.7	103 22	AAU54472 Antileukoprotease
87	26	86.7	103 22	AAU62439 Antileukoprotease
88	26	86.7	103 22	AAU44863 Antileukoprotease
89	26	86.7	103 22	AAU54472 Antileukoprotease
90	26	86.7	103 22	AAU62439 Antileukoprotease
91	26	86.7	103 22	AAU44863 Antileukoprotease
92	26	86.7	103 22	AAU54472 Antileukoprotease
93	26	86.7	103 22	AAU62439 Antileukoprotease
94	26	86.7	103 22	AAU44863 Antileukoprotease
95	26	86.7	103 22	AAU54472 Antileukoprotease
96	26	86.7	103 22	AAU62439 Antileukoprotease
97	26	86.7	103 22	AAU44863 Antileukoprotease
98	26	86.7	103 22	AAU54472 Antileukoprotease
99	26	86.7	103 22	AAU62439 Antileukoprotease
100	26	86.7	103 22	AAU44863 Antileukoprotease
101	26	86.7	103 22	AAU54472 Antileukoprotease
102	26	86.7	103 22	AAU62439 Antileukoprotease
103	26	86.7	103 22	AAU44863 Antileukoprotease
104	26	86.7	103 22	AAU54472 Antileukoprotease
105	26	86.7	103 22	AAU62439 Antileukoprotease
106	26	86.7	103 22	AAU44863 Antileukoprotease
107	26	86.7	103 22	AAU54472 Antileukoprotease
108	26	86.7	103 22	AAU62439 Antileukoprotease
109	26	86.7	103 22	AAU44863 Antileukoprotease
110	26	86.7	103 22	AAU54472 Antileukoprotease
111	26	86.7	103 22	AAU62439 Antileukoprotease
112	26	86.7	103 22	AAU44863 Antileukoprotease
113	26	86.7	103 22	AAU54472 Antileukoprotease
114	26	86.7	103 22	AAU62439 Antileukoprotease
115	26	86.7	103 22	AAU44863 Antileukoprotease
116	26	86.7	103 22	AAU54472 Antileukoprotease
117	26	86.7	103 22	AAU62439 Antileukoprotease
118	26	86.7	103 22	AAU44863 Antileukoprotease
119	26	86.7	103 22	AAU54472 Antileukoprotease
120	26	86.7	103 22	AAU62439 Antileukoprotease
121	26	86.7	103 22	AAU44863 Antileukoprotease
122	26	86.7	103 22	AAU54472 Antileukoprotease
123	26	86.7	103 22	AAU62439 Antileukoprotease
124	26	86.7	103 22	AAU44863 Antileukoprotease
125	26	86.7	103 22	AAU54472 Antileukoprotease
126	26	86.7	103 22	AAU62439 Antileukoprotease
127	26	86.7	103 22	AAU44863 Antileukoprotease
128	26	86.7	103 22	AAU54472 Antileukoprotease
129	26	86.7	103 22	AAU62439 Antileukoprotease
130	26	86.7	103 22	AAU44863 Antileukoprotease
131	26	86.7	103 22	AAU54472 Antileukoprotease
132	26	86.7	103 22	AAU62439 Antileukoprotease
133	26	86.7	103 22	AAU44863 Antileukoprotease
134	26	86.7	103 22	AAU54472 Antileukoprotease
135	26	86.7	103 22	AAU62439 Antileukoprotease
136	26	86.7	103 22	AAU44863 Antileukoprotease
137	26	86.7	103 22	AAU54472 Antileukoprotease
138	26	86.7	103 22	AAU62439 Antileukoprotease
139	26	86.7	103 22	AAU44863 Antileukoprotease
140	26	86.7	103 22	AAU54472 Antileukoprotease
141	26	86.7	103 22	AAU62439 Antileukoprotease
142	26	86.7	103 22	AAU44863 Antileukoprotease
143	26	86.7	103 22	AAU54472 Antileukoprotease
144	26	86.7	103 22	AAU62439 Antileukoprotease
145	26	86.7	103 22	AAU44863 Antileukoprotease
146	26	86.7	103 22	AAU54472 Antileukoprotease
147	26	86.7	103 22	AAU62439 Antileukoprotease
148	26	86.7	103 22	AAU44863 Antileukoprotease
149	26	86.7	103 22	AAU54472 Antileukoprotease
150	26	86.7	103 22	AAU62439 Antileukoprotease
151	26	86.7	103 22	AAU44863 Antileukoprotease
152	26	86.7	103 22	AAU54472 Antileukoprotease
153	26	86.7	103 22	AAU62439 Antileukoprotease
154	26	86.7	103 22	AAU44863 Antileukoprotease
155	26	86.7	103 22	AAU54472 Antileukoprotease
156	26	86.7	103 22	AAU62439 Antileukoprotease
157	26	86.7	103 22	AAU44863 Antileukoprotease
158	26	86.7	103 22	AAU54472 Antileukoprotease
159	26	86.7	103 22	AAU62439 Antileukoprotease
160	26	86.7	103 22	AAU44863 Antileukoprotease
161	26	86.7	103 22	AAU54472 Antileukoprotease
162	26	86.7	103 22	AAU62439 Antileukoprotease
163	26	86.7	103 22	AAU44863 Antileukoprotease
164	26	86.7	103 22	AAU54472 Antileukoprotease
165	26	86.7	1	

Pt¹ isolated nucleic acids and polypeptides, useful for preventing
 Pt¹ diagnosing and treating e.g. leukaemia, inflammation and immune
 disorders.
 Xx
 Ps Claim 20; SEQ ID NO 22103; 1399pp + Sequence Listing; English.
 Cc The invention relates to human poly nucleotides (AA179941-AM193841) and
 Cc the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 Cc cytokine, cell proliferation or cell differentiation or which may induce
 Cc production of other cytokines in other cell populations. The
 Cc polynucleotides and polypeptides are useful in gene therapy, vaccines or
 Cc peptide therapy. The polypeptides have various cytokine-like activities,
 Cc e.g. stem cell growth factor activity, haemopoiesis regulating
 Cc activity, tissue growth factor activity, immunomodulatory activity and
 Cc activity/inhibit activity and may be useful in the diagnosis and/or
 Cc treatment of cancer, leukaemia, nervous system disorders, arthritis and
 Cc inflammation.
 Note: The sequence data for this patent did not form part of the printed
 Cc specification, but was obtained in electronic format directly from WIPO
 Cc at ftp://wipo.int/pub/published_pct_sequences.
 Xx Sequence 87 AA;
 Query Match 100.0%; Score 30; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 58 YSQCR 62
 Result 2
 AAV28425
 Id AAV28425 standard; Protein: 243 AA.
 Xx
 Ac AAV28425;
 Xx
 Dt 15-FEB-2000 (first entry)
 Xx
 De Rice branched chain amino acid transaminase amino acid sequence.
 Xx
 Kw Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuc; leud;
 Kw branched chain amino acid transferase; biosynthetic enzyme; antibody;
 Kx 3-isopropylmalate dehydratase.
 Os Oryza sativa.
 Xx
 Pn WO9921880-A2.
 Xx
 Pd 05-MAY-1999.
 Xx
 Pp 20-OCT-1998; 98WO-US22081.
 Xx
 Pr 28-OCT-1997; 97US-003423.
 Xx
 Pa (DUPONT DU PONT DE NEMOURS & CO E I.
 Xx
 Pt FALCO SC, Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;
 Xx
 Dr WPI; 2000-022904/02.
 Dr N-FSDB; AAX89451.
 Xx
 Pt Nucleic acid fragments encoding branched chain amino acid biosynthetic
 Pt enzymes
 Xx
 Ps Claim 6; Fig 4; 102pp; English.
 Xx
 Cc AAV28419-Y2B431 are fragments of corn, soybean, wheat and rice branched
 Cc chain amino acid transaminase, amino acid sequences. Sequences
 Cc AAX89447-XB9465 are nucleic acid fragments that encode all or a
 Cc substantial portion of dihydroxyacid dehydratase, a branched chain amino
 Cc acid transferase, a leuc or a leud subunit of 3-isopropylmalate

Result 3
 AGI2153
 Id AGI2153 standard; Protein: 39 AA.
 Xx
 Ac AGI2153;
 Xx
 Dt 17-OCT-2000 (first entry)
 Xx
 De Arabidopsis thaliana protein fragment SEQ ID NO: 11153.
 Xx
 Kw Protein identification; signal transduction pathway; metabolic pathway;
 Kw hybridisation assay; genetic mapping; gene expression control; promoter;
 Kw termination sequence.
 Os Arabidopsis thaliana.
 Xx
 Pn EP1033405-A2.
 Xx
 Pd 06-SEP-2000.
 Xx
 Pr 25-FEB-2000; 2000EP-0301439.
 Xx
 Pr 25-FEB-1999; 99US-0121825.
 Pr 05-MAR-1999; 99US-0123180.
 Pr 09-MAR-1999; 99US-0123548.
 Pr 23-MAR-1999; 99US-0125788.
 Pr 25-MAR-1999; 99US-0126264.
 Pr 29-MAR-1999; 99US-0126785.
 Pr 01-APR-1999; 99US-0127462.
 Pr 06-APR-1999; 99US-0128234.
 Pr 08-APR-1999; 99US-0128714.
 Pr 16-APR-1999; 99US-0129845.
 Pr 19-APR-1999; 99US-0130077.
 Pr 21-APR-1999; 99US-0130449.
 Pr 23-APR-1999; 99US-0130510.
 Pr 23-APR-1999; 99US-0130891.
 Pr 28-APR-1999; 99US-0131449.
 Pr 30-APR-1999; 99US-0132208.
 Pr 30-APR-1999; 99US-0132407.
 Pr 04-MAY-1999; 99US-0132484.
 Pr 05-MAY-1999; 99US-0132485.
 Pr 05-MAY-1999; 99US-0132486.
 Pr 06-MAY-1999; 99US-0132487.
 Pr 07-MAY-1999; 99US-0132863.
 Pr 11-MAY-1999; 99US-0132865.
 Pr 14-MAY-1999; 99US-0134218.
 Pr 14-MAY-1999; 99US-0134219.
 Pr 14-MAY-1999; 99US-0134221.
 Pr 14-MAY-1999; 99US-0134370.
 Pr 18-MAY-1999; 99US-0134768.
 Pr 19-MAY-1999; 99US-0134941.
 Pr 20-MAY-1999; 99US-0135124.

PR	21-MAY-1999;	99US-013553.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135639.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-016592.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147202.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-017538.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138840.	PR	09-AUG-1999;	99US-0147335.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-019119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148365.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148884.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149166.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0149566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150864.
PR	18-JUN-1999;	99US-0139464.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139465.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151080.
PR	21-JUN-1999;	99US-0139817.	PR	30-AUG-1999;	99US-0151103.
PR	22-JUN-1999;	99US-0139829.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140353.	PR	01-SEP-1999;	99US-0151330.
PR	23-JUN-1999;	99US-0140354.	PR	07-SEP-1999;	99US-0151233.
PR	24-JUN-1999;	99US-0140395.	PR	10-SEP-1999;	99US-0151307.
PR	28-JUN-1999;	99US-0140823.	PR	13-SEP-1999;	99US-0151375.
PR	29-JUN-1999;	99US-0140891.	PR	15-SEP-1999;	99US-0151408.
PR	30-JUN-1999;	99US-0141287.	PR	16-SEP-1999;	99US-0151439.
PR	01-JUL-1999;	99US-0141842.	PR	20-SEP-1999;	99US-0151779.
PR	01-JUL-1999;	99US-0142154.	PR	22-SEP-1999;	99US-0151539.
PR	02-JUL-1999;	99US-0142055.	PR	23-SEP-1999;	99US-0151586.
PR	06-JUL-1999;	99US-0142390.	PR	24-SEP-1999;	99US-0151589.
PR	08-JUL-1999;	99US-0142803.	PR	28-SEP-1999;	99US-0151658.
PR	09-JUL-1999;	99US-0142920.	PR	29-SEP-1999;	99US-0151659.
PR	12-JUL-1999;	99US-0142977.	PR	04-OCT-1999;	99US-0151779.
PR	13-JUL-1999;	99US-0143521.	PR	05-OCT-1999;	99US-0151773.
PR	14-JUL-1999;	99US-0143624.	PR	06-OCT-1999;	99US-0151785.
PR	15-JUL-1999;	99US-0144005.	PR	07-OCT-1999;	99US-0151809.
PR	16-JUL-1999;	99US-0144085.	PR	08-OCT-1999;	99US-0151822.
PR	16-JUL-1999;	99US-0144086.	PR	12-OCT-1999;	99US-0151836.
PR	19-JUL-1999;	99US-0144087.	PR	13-OCT-1999;	99US-0151923.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0151924.
PR	19-JUL-1999;	99US-0144334.	PR	13-OCT-1999;	99US-0151925.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0151932.
PR	19-JUL-1999;	99US-0144336.	PR	14-OCT-1999;	99US-0151933.
PR	20-JUL-1999;	99US-0144337.	PR	14-OCT-1999;	99US-0151937.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-01519637.
PR	21-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-01519638.
PR	21-JUL-1999;	99US-0145085.	PR	18-OCT-1999;	99US-01519584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	23-JUL-1999;	99US-0145218.	PR	21-OCT-1999;	99US-0160767.
PR	23-JUL-1999;	99US-0145224.	PR	21-OCT-1999;	99US-0160768.
PR	23-JUL-1999;	99US-0145275.	PR	21-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	22-JUL-1999;	99US-0145089.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145192.	PR	26-OCT-1999;	99US-0161359.
PR	27-JUL-1999;	99US-0145145.	PR	26-OCT-1999;	99US-0161360.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.			

PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161921.
 PR 29-OCT-1999; 99US-0161933.

Query Match, Best Local Similarity 80.0%;保守性 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSQCR 5
 DB 14 YNQCR 18

RESULT 4
 ABG16866
 ID AAG76769 standard; Protein; 52 AA.
 AC XX
 AC AAG76769;
 DT 03-SEP-2001 (first entry)
 DE Human colon cancer antigen protein SEQ ID NO:7533.
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 PD 05-APR-2001.
 XX
 PP 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-015137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 DR WPI; 2001-235357/24.
 DR N-PSDB; AAH36174.

Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PT Claim 11: Page 8951-8952; 9103pp; English.

XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytotoxic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID No:1027 to 1052, 7921 and 7922.

SQ Sequence 52 AA;

Query Match, Best Local Similarity 80.0%;保守性 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSQCR 5
 DB 29 YNQCR 33

RESULT 5
 ABG16866
 ID ABG16866 standard; Protein; 92 AA.
 AC XX
 AC ABC16866;
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #16857.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PP 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0549217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS81053.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX
 PS Claim 20, SEQ ID No 47225; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABC0010-ABC0377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/pct/published-pct.html>.
 XX
 SQ Sequence 92 AA;

Query Match, Best Local Similarity 80.0%;保守性 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQCR 5
 ||||:
 CC
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

RESULT 6
 AAB40523
 ID AAB40523 standard; Protein: 124 AA.
 XX
 AC AAB40523;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORF8X ORF287 polypeptide sequence SEQ ID NO:574.
 XX
 KW Human; open reading frame; ORF8X; detection; cytostatic; hepatotropic;
 KW cardiovascular; antiviral; antipapillomavirus; immunosuppressive; antiinflammatory;
 KW immunomodulator; antitumour; antineoplastic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antifungal; antirheumatic; antihypertension;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection; DE
 KW severe; combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW bone damage; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 31-MAR-2000; 2000W0-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 XX
 DR N-PSDB; AAC74732.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 useful for treating e.g. cancers, proliferative disorders,
 neurodegenerative disorders and cardiovascular disease -
 XX
 Claim 11; Page 719; 5507pp; English.
 XX
 ACT4446 to AAC77605 encode the proteins given in AAB40237 to AAB43397,
 which represent the human ORF8 open reading frames 1 to 3161. The ORF8
 sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 osteopathic; antipapillomavirus; antiarthritic; immunosuppressive;
 immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 antiinflammatory; antibacterial; antiviral; immunosuppressive;
 antifungal; antirheumatic; antihypertension; antidiabetic; antineoplastic;
 antithyroid; and antianemic. The sequences can be used for determining
 the presence of or predisposition to, or preventing or treating
 pathological conditions associated with an ORF8-associated disorder. The
 nucleic acids can be used to express ORF8 proteins in gene therapy
 vectors. The proteins and nucleic acids may be used to treat cancers,
 proliferative disorders, neurodegenerative disorders, osteoarthritis,
 graft vs host disease, cardiovascular disease, diabetes mellitus,
 hypertension, hypothyroidism, cholesterol ester storage, systemic lupus

CC erythematous, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

RESULT 7
 ABP31173
 ID ABP31173 standard; Protein: 124 AA.
 XX
 AC ABP31173;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Human ORF146 protein, SEQ ID NO:292.
 XX
 Human; ORF; open reading frame; ORF8X; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haemopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
 KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; viricide; antibacterial; fungicide.
 XX
 OS Homo sapiens.
 XX
 PN WO200190366-A2.
 XX
 PD 29-NOV-2001.
 XX
 PR 24-MAY-2000; 2000US-0517076.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Leach MD, Shinkets RA;
 XX
 PS WPI; 2002-106700/14.
 DR N-PSDB; ABN75199.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 preventing and treating cardiovascular disease, neurodegenerative,
 hyperproliferative disorders and disorders related to organ
 transplantation -
 XX
 PS Claim 10; Page 342; 250pp; English.
 XX
 CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN7054-
 CC ABN9587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORF8) proteins, polynucleotides at least 85% identical to
 CC the ORF8 nucleic acid sequences, vectors and host cells comprising ORF8
 CC polynucleotides, the recombinant production of ORF8 proteins, antibodies
 specific for ORF8 proteins, methods of detecting ORF8 polynucleotides and

CC polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haemopoiesis regulation, tissue growth, angiogenesis, actin or inhibit activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiviral activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins which are useful as immunogens to generate specific antibodies may also be used as diagnostics, treatment and monitoring of ORFX-associated diseases.

SQ Sequence 124 AA:

Query Match^{90.0%}; Score 27; DB 23; Length 124;
Best Local Similarity 80.0%; Pred. No. 7e-02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; QY 1 YSQCR 5
QY |:||| Db 110 YAQCR 114

RESULT 8
AAW59178 Standard; Protein: 134 AA.

QY 1 YSQCR 5
Db 110 YAQCR 114

RESULT 9
AAW59178 Standard; Protein: 153 AA.

QY 1 YSQCR 5
Db 94 YTQCR 98

CC for the treatment of diseases.
XX

CC Sequence 134 AA:
SQ

Query	Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	1 YSQCR 5	80.0%	27	19	134	0	0
Db	94 YTQCR 98						

RESULT 9
ABG09610 ABG09610 standard; Protein: 153 AA.

CC ID ABG09610:
XX AC ABC09610:
XX NC AC

CC DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #9601.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic; KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.

XX PN WO200175067-A2.
XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX DR 23-AUG-2000; 2000US-0649167.

XX PA N-PSDB; AAS73797.

XX PT (HYSE-) HYSEQ INC.

XX PI Dimanac RT, Liu C, Tang YT;

XX DR WPI; 2001-539362/73.

XX PS Claim 20; SEQ ID NO 39969; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABC0010-ABC0377 represent novel human
CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at fp.wipo.int/pub/published-pct/sequences.

CC New DNA coding rat-derived eosinophil cationic protein - used, e.g.
PT to produce recombinant protein for treatment of diseases
XX Claim 1; Page 12; 14pp; Japanese.

CC This sequence is a novel rat-derived eosinophil cationic protein (ECP)
CC which exhibits cytotoxic activity. The DNA encoding the ECP protein
CC can be used for the production of recombinant protein which is useful

SQ	Sequence	153 AA.	OS	Rattus sp.
QY	Query Match 90.0%; Score 27; DB 22; Length 153;	XX	XX	
	Best Local Similarity 80.0%; Pred. No. 8.3e+02;	PN	JP11009280-A.	
	Matches 4; Conservative 1; Mismatches 0;	XX	XX	
	Indels 0; Gaps 0;	PD	19-JAN-1999.	
QY	1 YSQCR 5 :	XX	PF	25-JUN-1997; 97JP-0169271.
Db	59 YAOQR 63	XX	XX	25-JUN-1997; 97JP-0169271.
RESULT 10				
AAM59177		XX	PA	(NIH) JAPAN ENERGY CORP.
ID AAM59177	standard; Protein; 155 AA.	XX	XX	
XX		DR	WPI; 1999-145897/13.	
AC AAM59177;		DR	N-PSDB; AAX05636, AAX05637.	
XX		XX	New rat-derived eosinophil-derived neurotoxin gene - useful for	
DT 13-AUG-1998	(first entry)	PT	preparing recombinant protein	
XX		PS	Claim 1; Page 10; 18pp; Japanese.	
DE Rat eosinophil cationic protein #1.		XX	This represents a rat-derived eosinophil-derived neurotoxin (EDN). The	
XX		CC	DNA coding rat-derived EDN or its precursor peptide is useful for the	
KW Eosinophil cationic protein; ECP; cytotoxic; recombinant protein;		CC	preparation of a recombinant protein. The base sequence of a precursor	
KW treatment; disease; rat.		CC	peptide of rat eosinophils-derived eosinophil cationic protein (ECP),	
OS Rattus sp.		CC	and the base sequence of the precursor peptide of EDN can be determined	
XX PN JPI011777-A.		CC	by collecting the ECP cDNA and EDN cDNA from eosinophils respectively.	
XX		SQ	Sequence 155 AA;	
PD 12-MAY-1998.		QY	Query Match 90.0%; Score 27; DB 20; Length 155;	
XX 25-OCT-1996; 96JP-0284311.		DB	Best Local Similarity 80.0%; Pred. No. 8.4e+02;	
XX 25-OCT-1996; 96JP-0284311.		XX	Matches 4; Conservative 1; Mismatches 0;	
PA (NIH) JAPAN ENERGY CORP.		XX	Indels 0; Gaps 0;	
XX WPI; 1998-35891/29.		XX		
DR N-PSDB; AAV11934, AAV11935.		XX		
XX		RESULT 12		
PT New DNA coding rat-derived eosinophil cationic protein - used, e.g.		AAM94273		
PT to produce recombinant protein for treatment of diseases		ID AAM94273 standard; Protein; 155 AA.		
PS Claim 3, Page 9-10; 14pp; Japanese.		XX		
XX		AC AAM94273;		
CC This sequence is a novel rat-derived eosinophil cationic protein (ECP)		XX		
CC which exhibits cytotoxic activity. The DNA encoding the ECP protein		DT 22-APR-1999	(first entry)	
CC can be used for the production of recombinant protein which is useful		XX		
CC for the treatment of diseases.		DE Rat eosinophils-derived eosinophil cationic protein (ECP).		
XX Sequence 155 AA;		XX		
QY Query Match 90.0%; Score 27; DB 19; Length 155;		KW Eosinophil-derived neurotoxin; EDN; eosinophil cationic protein; ECP;		
Best Local Similarity 80.0%; Pred. No. 8.4e+02;		KW recombinant; rat; precursor.		
Matches 4; Conservative 1; Mismatches 0;		OS Rattus sp.		
Db 1 YSQCR 5 :		XX		
Db 115 YTQCR 119		FT Key	Location/Qualifiers	
XX		FT Peptide	59 /note= "indicated as Cys in the sequence listing"	
XX		FT Peptide	.99 /note= "indicated as Val in the sequence listing"	
XX		FT Peptide	/note= "indicated as Val in the sequence listing"	
XX		PN JPI11009280-A.		
XX		XX		
XX		PD 19-JAN-1999.		
XX		XX		
XX		PF 25-JUN-1997; 97JP-0169271.		
AC AAM94272;		XX		
XX		PF 25-JUN-1997; 97JP-0169271.		
AC AAM94272;		XX		
XX 22-APR-1999	(first entry)	PR .		
XX		XX		
DE Rat-derived eosinophil-derived neurotoxin (EDN).		PA (NIH) JAPAN ENERGY CORP.		
XX		XX		
KW Eosinophil-derived neurotoxin; EDN; eosinophil cationic protein; ECP;		DR WPI; 1999-145897/13.		
KW recombinant; rat; precursor.		DR N-PSDB; AAX05638.		
XX		PT New rat-derived eosinophil-derived neurotoxin gene - useful for		

PT preparing recombinant protein
 XX disclosure; Fig 4; 18pp; Japanese.

CC This represents a rat eosinophils-derived eosinophil cationic protein (EDN) (PCT). The DNA encoding a rat-derived eosinophil-derived neurotoxin (EDN) or its precursor peptide is useful for the preparation of a recombinant protein. The base sequence of a precursor peptide of rat eosinophil-derived ECP, and the base sequence of the precursor peptide of EDN can be determined by collecting the ECP cDNA and EDN cDNA from eosinophils respectively.

CC Sequence 155 AA;

Query	Match	Similarity	Score	DB	Length
Best	Local	80.0%	27	20;	155;
Matches			Pred. No.	8.4e+02;	
Qy	1	VSOQR 5	1;	Mismatches	0;
Db	115	YRQCR 119	Indels	0;	Gaps 0;

XX

RESULT 13

ID ABBG13128 standard; Protein: 187 AA.

XX

AC ABBG13128;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #13119.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PR 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US 0649167.

XX

PA (HYSE*) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639352/73.

DR N-PSDB; AAS77315.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX

PS Claim 20; SEQ ID NO 43487; 103pp; English.

XX

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

CC Sequence 187 AA;

Query	Match	Similarity	Score	DB	Length
Best	Local	80.0%	27	22;	187;
Matches			Pred. No.	9.9e+02;	
Qy	1	VSOQR 5	1;	Mismatches	0;
Db	140	YSQCK 144	Indels	0;	Gaps 0;

XX

RESULT 14

ID ABB58567 standard; Protein: 320 AA.

XX

AC ABB58567;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 2493.

XX

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PR 23-MAR-2001; 2001WO-US09231.

XX

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX

(PEKE) PE CORP NY.

XX

PI Venter JC, Adams M, Li PW, Myers EW;

XX

DR WPI; 2001-656860/75.

DR N-PSDB; ABL02670.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

XX

PS Disclosure; SEQ ID NO 2493; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB0101840-ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5777-ABB7072).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX

SQ Sequence 320 AA;

Query	Match	Similarity	Score	DB	Length
90.0%	27	DB 22;	Length 320;		

PR 12-AUG-1999; 990S-0148341.
 PR 13-AUG-1999; 990S-0148665.
 PR 16-AUG-1999; 990S-0148684.
 PR 17-AUG-1999; 990S-0149368.
 PR 18-AUG-1999; 990S-0149426.
 PR 20-AUG-1999; 990S-0149722.
 PR 20-AUG-1999; 990S-0149723.
 PR 23-AUG-1999; 990S-0149929.
 PR 23-AUG-1999; 990S-0149902.
 PR 25-AUG-1999; 990S-0150566.
 PR 26-AUG-1999; 990S-0150884.
 PR 27-AUG-1999; 990S-0151065.
 PR 27-AUG-1999; 990S-0151066.
 PR 30-AUG-1999; 990S-0151080.
 PR 31-AUG-1999; 990S-0151303.
 PR 01-SEP-1999; 990S-0151438.
 PR 07-SEP-1999; 990S-0151930.
 PR 10-SEP-1999; 990S-0152363.
 PR 13-SEP-1999; 990S-0153070.
 PR 27-AUG-1999; 990S-0153758.
 PR 15-SEP-1999; 990S-0154018.
 PR 16-SEP-1999; 990S-0154039.
 PR 20-SEP-1999; 990S-0154779.
 PR 22-SEP-1999; 990S-0155139.
 PR 23-SEP-1999; 990S-0155486.
 PR 24-SEP-1999; 990S-0155659.
 PR 28-SEP-1999; 990S-0156458.
 PR 29-SEP-1999; 990S-0156596.
 PR 04-OCT-1999; 990S-0157117.
 PR 05-OCT-1999; 990S-0157753.
 PR 06-OCT-1999; 990S-0157865.
 PR 07-OCT-1999; 990S-0158029.
 PR 08-OCT-1999; 990S-0158232.
 PR 12-OCT-1999; 990S-015859.
 PR 13-OCT-1999; 990S-0159293.
 PR 13-OCT-1999; 990S-0159294.
 PR 14-OCT-1999; 990S-0159325.
 PR 14-OCT-1999; 990S-0159329.
 PR 14-OCT-1999; 990S-0159330.
 PR 14-OCT-1999; 990S-0159331.
 PR 14-OCT-1999; 990S-0159637.
 PR 18-OCT-1999; 990S-0159584.
 PR 21-OCT-1999; 990S-0160741.
 PR 21-OCT-1999; 990S-0160767.
 PR 21-OCT-1999; 990S-0160768.
 PR 21-OCT-1999; 990S-0160770.
 PR 25-OCT-1999; 990S-0161404.
 PR 25-OCT-1999; 990S-0161405.
 PR 26-OCT-1999; 990S-0161406.
 PR 26-OCT-1999; 990S-0161359.
 PR 26-OCT-1999; 990S-0161360.
 PR 28-OCT-1999; 990S-0161361.
 PR 28-OCT-1999; 990S-0161920.
 PR 28-OCT-1999; 990S-0161922.
 PR 29-OCT-1999; 990S-016193.
 PR 29-OCT-1999; 990S-0162142.

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 Job time : 23 secs

Query Match 90.0%; Score 27; DB 21; Length 424;
 Best Local Similarity 80.0%; Pred. No. 2e03; Mismatches 1; Indels 0; Caps 0;
 Matches 4; Conservative 1; MisMatches 0;

Qy 1 YSSCR 5
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 Db 10 YSSCR 14

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Sequence: 1 YSQCR 5

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cn2_6/potdata/1/1aa/Packfiles1.pep:*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	30	100.0	243	4	US-09-173-300-22
2	27	90.0	1693	3	US-08-840-316-1
3	27	90.0	1693	3	US-08-478-507-7
4	27	90.0	1693	4	US-08-809-523-1
5	27	90.0	1693	4	US-09-275A-7
6	27	90.0	1693	4	US-08-471-971-1
7	27	90.0	1693	4	US-09-553-427-7
8	27	90.0	1693	4	US-09-402-776-1
9	27	90.0	1693	5	PCT-US93-08849A-1
10	27	90.0	1693	4	PCT-US93-08849-1
11	27	90.0	1708	4	US-09-462-606-2
12	26	86.7	32	1	US-09-361-920-10
13	26	86.7	32	1	US-08-479-939-10
14	26	86.7	32	1	US-08-483-432-10
15	26	86.7	47	2	US-09-464-182A-27
16	26	86.7	47	2	US-08-274A-16
17	26	86.7	47	2	US-08-406-271-27
18	26	86.7	108	3	US-08-959-212-10
19	26	86.7	155	1	US-08-150-203A-9
20	26	86.7	155	1	US-08-454-730-9
21	26	86.7	155	4	US-09-949-788-9
22	26	86.7	216	4	US-09-556-877-20
23	26	86.7	216	4	US-09-288-594A-20
24	26	86.7	216	4	US-09-620-412C-20
25	26	86.7	291	4	US-08-560-098A-55
26	86.7	295	4	US-09-799-345-2	
27	86.7	349	3	US-08-651-136C-10	

ALIGNMENTS

```

RESULT 1
; Sequence 22, Application US/09173300
; Patent No. 6451581
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Canoon, Rebecca E.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1126
; CURRENT APPLICATION NUMBER: US/09-173-300
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 60/063,423
; EARLIER FILING DATE: 1997 October 28
; NUMBER OF SEQ 'ID' NOS: 54
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO: 22
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Glycine max
US-09-173-300-22
; US-09-173-300-22
Query Match 100.0%; Score: 30; DB: 4; Length: 243;
Best Local Similarity: 100.0%; Pred. No.: 86; Mismatches: 0; Indels: 0; Gaps: 0;
Matches: 5; Conservative: 0; Number of保守氨基酸对数: 0;
Oy 1 YSQCR 5
Db 68 YSQCR 72

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RESULT 2
; Sequence 1, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H., Tsvarev, Sergei A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of Hepatitis E And Their Use In Diagnostic Methods And Vaccines
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNIGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA

ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/840,316
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Richard W. Bork
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4255
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEX/FAX: (212) 751-6949
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1693 AMINO ACID RESIDUES
 TYPE: AMINO ACID
 STRANDEDNESS: UNKNOWN
 TOPOLOGY: UNKNOWN
 ;
 US-08-840-316-1

Query Match 90.0%; Score 27; DB 3; Length 1693;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VSQCR 5
 Db 431 YAQCR 435

RESULT 3
 US-08-478-507-7
 ; Sequence 7, Application US/08478507
 ; Patent No. 6120988
 ; GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R
 APPLICANT: Yarbrough, Patrice O
 APPLICANT: Bradley, Daniel W
 APPLICANT: Krawczyński, Krzysztof Z
 APPLICANT: Tam, Albert
 APPLICANT: Fry, Kirk E
 TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
 TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478,507
 FILING DATE: 07-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/279,823
 FILING DATE: 25-JUL-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/681,078
 FILING DATE: 05-APR-1991

RESULT 4
 US-08-809-523-1
 ; Sequence 1, Application US/08809523
 ; Patent No. 6207416
 ; GENERAL INFORMATION:
 APPLICANT: Tsvarev, Sergei A.; Emerson,
 APPLICANT: Suzanne U.; Purcell, Robert H.
 TITLE OF INVENTION: Recombinant Proteins Of
 TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
 TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,523
 FILING DATE: 28-MAY-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13102
 FILING DATE: 03-OCT-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/316,765
 FILING DATE: 03-OCT-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/947,263

FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
;US-08-809-523-1

Query Match Similarity 90.0%; Score 27; DB 4; Length 1693;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0;
Matches 4; Conservative 1; Indels 0; Gaps 0;
QY 1 YSQCR 5
Db 431 YAOCR 435

RESULT 5
US-09-128-275A-7
; Sequence 7, Application US/09128275A
; Patent No. 6229005
GENERAL INFORMATION:
APPLICANT: Reves, Gregory R
APPLICANT: Yarboough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: FRY, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6229005-A/No. 6229005-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
ZIP: 94306
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,275A
FILING DATE: 03-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:

RESULT 6
US-08-471-971-1
; Sequence 1, Application US/08471971
; Patent No. 6287759
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADRESSEEE: MORGAN & FINNEGANS
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,971
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN

; US-08-471-971-1
TOPOLOGY: UNKNOWN

;

Query Match 90.0%; Score 27; DB 4; Length 1693;

Best Local Similarity 80.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 0;

Indels 0; Gaps 0;

Oy 1 YSOCR 5
|:|||
Db 431 YAOCR 435

RESULT 7

; DS-09-553-427-7
Sequence 7, Application US/09553427

Patent No. 6379891

GENERAL INFORMATION:

APPLICANT: Reyes, Gregory R

APPLICANT: Yarborough, Patrice O

APPLICANT: Bradley, Daniel W

APPLICANT: Kruczynski, Krzysztof Z

APPLICANT: Tam, Albert

APPLICANT: FRY, Kirk E

TITLE OF INVENTION: DNA Sequences of Enterically Transmitted

NUMBER OF SEQUENCES: 20 TITLE OF INVENTION: No. 6379891-A/No. 6379891-B Hepatitis Viral Agent

CORRESPONDENCE ADDRESS:

ADDRESSEE: Behlberger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentnet Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/553,427

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/478,507

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/279,823

FILING DATE: 25-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/553,421

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/505,888

FILING DATE: 05-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/420,921

FILING DATE: 13-OCT-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/367,486

FILING DATE: 16-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/336,672

FILING DATE: 11-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/208,997

FILING DATE: 17-JUN-1988

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600-0183.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324 0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1693 AMINO ACID RESIDUES

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

; US-09-402-776-1
Sequence 1, Application US/09402776

GENERAL INFORMATION:

Patent No. 6458562

APPLICANT: Emerson, Suzanne U., Purcell, Robert H., Tsvare, Sergei A., and Robinson, Robin A.

TITLE OF INVENTION: Recombinant Proteins Of A Pakistani Strain Of Hepatitis E And Their Use In Diagnostic Methods And Vaccines

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,776

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/840,316

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Richard W. Bork

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4255

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-8800

TELEFAX: (212) 751-6849

US-09-402-776-1

Query Match 90.0%; Score 27; DB 4; Length 1693;

Best Local Similarity 80.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 0;

Indels 0; Gaps 0;

Oy 1 YSOCR 5
|:|||
Db 431 YAOCR 435

RESULT 9

PCT-US93-08849A-1

; sequence 1, Application PC/TUS9308849A,

; GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 54570460 No. 5457046th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/351,920

FILING DATE: 09-MAY-1990

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/940, 860

FILING DATE: 28-OCT-1992

APPLICATION NUMBER: DK 1158/90

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00124

FILING DATE: 08-MAY-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: 3435. 204-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123

TELEFAX: 212-867-0298

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids

REFERENCE/DOCKET NUMBER: 3435. 204-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123

TELEFAX: 212-867-0298

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: Peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:
 ORGANISM: Fusarium oxysporum

US-08-361-920-10

Query Match 86.7%; Score 26; DB 1; Length 32;
 Best Local Similarity 80.0%; Pred. No. 83; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
 ||||:
 Db 28 YSQCQ 32

RESULT 13

US-08-479-939-10

Sequence 10, Application US/08479939

GENERAL INFORMATION:
 GENERAL NO. 5686593

APPLICANT: Woeldike, Helle F.

APPLICANT: Hagen, Frederick

APPLICANT: Hjort, Carsten M.

APPLICANT: Sven, Hastrup

TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,432

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: Peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:
 ORGANISM: Fusarium oxysporum

US-08-479-939-10

Query Match 86.7%; Score 26; DB 1; Length 32;
 Best Local Similarity 80.0%; Pred. No. 83; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
 ||||:
 Db 28 YSQCQ 32

RESULT 14

US-08-483,432-10

Sequence 10, Application US/08483432

Patent No. 5763254

GENERAL INFORMATION:
 APPLICANT: Woeldike, Helle F.

APPLICANT: Hagen, Frederick

APPLICANT: Hjort, Carsten M.

APPLICANT: Sven, Hastrup

TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,432

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,920
 FILING DATE: 09-MAY-1990
 APPLICATION NUMBER: US 07/940,860
 FILING DATE: 28-OCT-1992
 APPLICATION NUMBER: DK 1158/90
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00124
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 3435.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0233
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Fusarium oxysporum
 US-08-483-432-10

Query Match 86.7%; Score 26; DB 1; Length 32;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
 ||||:
 Db 28 YSQCQ 32

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 Job time : 13.25 secs

RESULT 15
 US-08-464-182A-27
 Sequence 27, Application US/08464182A
 ; Patent No. 5849885
 GENERAL INFORMATION:
 APPLICANT: Nuijens, Jan H.
 TITLE OF INVENTION: Isolation of Lactoferrin from Milk
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,182A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/406,271
 FILING DATE: 09-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/198,321
 FILING DATE: 16-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 016994-004920US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 326-2400
 TELEFAX: (650) 326-2422
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 47 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..47
 OTHER INFORMATION: /note= "PLF"
 US-08-464-182A-27

Query Match 86.7%; Score 26; DB 2; Length 47;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 ||||:
 Db 16 YSKCR 20

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 (without alignments)
 28.746 Million cell updates/sec

Title: US-09-851-058-2

Perfect score: 30

Sequence: 1 YSQCR 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/1/pubpaas/US05_PUCOMB_pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	100.0	243	12 US-10-027-450-22
2	27	90.0	52	9 US-10-056-698-7543
3	27	90.0	1693	9 US-09-851-10-7
4	27	90.0	1698	9 US-09-468-147-91
5	27	90.0	1708	9 US-09-464-147-165
6	26	86.7	1708	10 US-09-854-761-2491
7	26	86.7	103	10 US-09-854-761-2491
8	26	86.7	114	10 US-09-925-300-1551
9	26	86.7	199	10 US-09-734-569-130
10	26	86.7	216	10 US-09-841-132-20
11	26	86.7	253	10 US-09-925-300-1601
12	26	86.7	289	9 US-09-738-626-5525
13	26	86.7	295	10 US-09-952-276-2
14	26	86.7	349	9 US-10-007-521-10
15	26	86.7	356	9 US-10-567-601-8811
16	26	86.7	377	9 US-10-104-880-8
17	26	86.7	381	9 US-10-052-032-29
18	26	86.7	420	10 US-09-853-386-129
19	26	86.7	424	9 US-09-853-450-16
20	26	86.7	591	10 US-09-815-242-5562
21	26	86.7	1000	9 US-09-823-187-6
22	26	83.3	25	9 US-09-802-152-152
23	25	83.3	30	10 US-09-917-340-449
24	25	83.3	31	9 US-09-916-494A-2
25	25	83.3	33	9 US-09-916-494A-6
26	25	83.3	34	7 US-08-841-636A-37
27	25	83.3	34	12 US-09-001-843-205
28	25	83.3	39	9 US-09-916-494A-4
29	25	83.3	40	9 US-10-125-258-103
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32	25	83.3	46	9 US-10-073-961-283
33	25	83.3	46	10 US-09-764-887-283
34	25	83.3	52	9 US-09-983-802-001
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38	25	83.3	71	9 US-10-083-357-763
39	25	83.3	73	10 US-09-864-761-40832
40	25	83.3	102	8 US-08-42-550B-4
41	25	83.3	141	9 US-10-101-464A-91
42	25	83.3	144	9 US-10-156-761-11527
43	25	83.3	145	10 US-09-893-731-88
44	25	83.3	156	9 US-09-907-969-586
45	25	83.3	156	9 US-10-198-053-586

ALIGNMENTS

RESULT 1

US-10-027-450-22

; Sequence 22, Application US/10027450
; Sequence 22, Application US/10027450
; Patent No. US20020102715A1

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio, Carl

; APPLICANT: Hitz, William, D.

; APPLICANT: Kinney, Anthony, J.

; APPLICANT: Cahoon, Rebecca, E.

; APPLICANT: Rafalski, J., Antoni

; TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES

; FILE REFERENCE: BB-1126

; CURRENT APPLICATION NUMBER: US/10/027,450

; CURRENT FILING DATE: 2001-12-20

; PRIORITY APPLICATION NUMBER: 60/053,423

; PRIOR FILING DATE: 1997 October 28

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: Microsoft Word Version 7.0A

; SEQ ID NO 22

; LENGTH: 243

; TYPE: PRT

; ORGANISM: Glycine max

; US-10-027-450-22

Query Match Best Local Similarity 100.0%; Score 30; DB 12; Length 243; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQCR 5

Db 68 YSQCR 72

RESULT 2

US-10-106-698-7543

; Sequence 7543, Application US/10106698

; Publication No. US/2003/0109690A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept

; FILE REFERENCE: PA005P1

; CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27
 PRIORITY APPLICATION NUMBER: PCT/US00/26524
 PRIORITY FILING DATE: 2000-09-28
 PRIORITY APPLICATION NUMBER: US 60/157,137
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO: 7543
 LENGTH: 52
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-698-7543

Query Match 90.0%; Score 27; DB 9; Length 52;
 Best Local Similarity 80.0%; Pred. No. 1.1e-02; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 QY 1 YSOCCR 5
 Db 29 YNQCR 33

RESULT 3
 US-09-851-410-7
 Sequence 7, Application US/09851410
 Publication No. US20030124510A1
 GENERAL INFORMATION:
 APPLICANT: Reves, Gregory R
 Yabough, Parrice O
 Bradley, Daniel W
 Kowczynski, Krzysztof Z
 Tam, Albert
 Fry, Kirk E
 TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
 NO. US2003014510A1-A/NO. US20030124510A1-B Hepatitis Viral
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/M-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/851,410
 FILING DATE: 07-MAY-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/128,275
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 07/681,078
 FILING DATE: 05-APR-1991
 APPLICATION NUMBER: US 07/505,888
 FILING DATE: 05-APR-1990
 APPLICATION NUMBER: US 07/420,921
 FILING DATE: 13-OCT-1989
 APPLICATION NUMBER: US 07/367,486
 FILING DATE: 16-JUN-1989
 APPLICATION NUMBER: US 07/7336,672
 FILING DATE: 11-APR-1989
 APPLICATION NUMBER: US 07/208,997
 FILING DATE: 17-JUN-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Petitory, Joanne R.
 REGISTRATION NUMBER: 42,995
 REFERENCE/DOCKET NUMBER: 4600-0183.24
 TELECOMMUNICATION INFORMATION:

Query Match 90.0%; Score 27; DB 9; Length 1693;
 Best Local Similarity 80.0%; Pred. No. 2.6e+03; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 QY 1 YSOCCR 5
 Db 431 YACQR 435

RESULT 4
 US-09-468-147-91
 Sequence 91, Application US/09468147A
 Publication No. US20030049601A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Schlauder, George G.
 APPLICANT: Desai, Suresh M.
 APPLICANT: Dawson, George J.
 APPLICANT: Mushahwar, I. K.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 FILE REFERENCE: 6232.US.P1
 CURRENT APPLICATION NUMBER: US/09/468,147A
 EARLIER FILING DATE: 1999-11-21
 EARLIER FILING DATE: 1998-10-15
 EARLIER APPLICATION NUMBER: US 60/061,199
 EARLIER FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 258
 SOFTWARE: FASTSEQ For Windows Version 3.0
 SEQ ID NO: 91
 LENGTH: 1698
 TYPE: PRT
 ORGANISM: Hepatitis E Virus

FEATURE:
 OTHER INFORMATION: Xaa = Unknown or Other at position 174
 OTHER INFORMATION: Xaa = Unknown or Other at position 363
 OTHER INFORMATION: Xaa = Unknown or Other at position 1088
 OTHER INFORMATION: Xaa Unknown or Other at position 1131
 OTHER INFORMATION: Xaa = Unknown or Other at position 1217
 OTHER INFORMATION: Xaa = Unknown or Other at position 1389

Query Match 90.0%; Score 27; DB 9; Length 1698;
 Best Local Similarity 80.0%; Pred. No. 2.6e+03; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 QY 1 YSOCCR 5
 Db 422 YAQCR 426

RESULT 5
 US-09-468-147-166
 Sequence 156, Application US/09468147A
 Publication No. US2003049601A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Schlauder, George G.
 APPLICANT: Desai, Suresh M.

APPLICANT: Dawson, George J.
 APPLICANT: Mushtawar, I. K.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
 TITLE OF INVENTION: HEPATITIS E VIRUS
 FILE REFERENCE: 6232.US.P1
 CURRENT FILING DATE: 1999-12-21
 EARLIER APPLICATION NUMBER: US 09/173,141
 EARLIER FILING DATE: 1998-10-15
 EARLIER APPLICATION NUMBER: US 60/061,199
 EARLIER FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 258
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 166
 LENGTH: 1708
 TYPE: PRT
 ORGANISM: Hepatitis E Virus
 FEATURE:
 OTHER INFORMATION: Xaa = Unknown or Other at position 322
 OTHER INFORMATION: Xaa = Unknown or Other at position 331
 OTHER INFORMATION: Xaa = Unknown or Other at position 445
 OTHER INFORMATION: Xaa = Unknown or Other at position 448
 OTHER INFORMATION: Xaa = Unknown or Other at position 634
 OTHER INFORMATION: Xaa = Unknown or Other at position 646
 OTHER INFORMATION: Xaa = Unknown or Other at position 811
 OTHER INFORMATION: Xaa = Unknown or Other at position 1553
 OTHER INFORMATION: Xaa = Unknown or Other at position 1578
 OTHER INFORMATION: Xaa = Unknown or Other at position 1691
 ; US-09-468 147-166

Query Match 90.0%; Score 27; DB 9; Length 1708;
 Best Local Similarity 80.0%; Pred. No. 2.6e+03; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 VSQCR 5
 ||:||
 Db 431 YACQR 435

RESULT 6
 US-09-864-761-42491
 ; Sequence 42491, Application US/09864761
 ; Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wenheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Reonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30

Query Match 90.0%; Score 27; DB 9; Length 1708;
 Best Local Similarity 80.0%; Pred. No. 2.6e+03; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 VSQCR 5
 ||:||
 Db 431 YACQR 435

RESULT 6
 US-09-864-761-42491
 ; Sequence 42491, Application US/09864761
 ; Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wenheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Reonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30

Query Match 90.0%; Score 27; DB 9; Length 1708;
 Best Local Similarity 80.0%; Pred. No. 2.6e+03; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0;

Qy 1 VSQCR 5
 ||:||
 Db 431 YACQR 435

RESULT 7
 US-09-925-300-1551
 ; Sequence 1551, Application US/09925300
 ; Patent No. US20020151681A1
 GENERAL INFORMATION:
 APPLICANT: Craig Rosen,
 APPLICANT: Steve Ruben,
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05988
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1998-03-12
 NUMBER OF SEQ ID NOS: 1890
 SOFTWARE: RatatIn Ver. 2.0
 SEQ ID NO: 1551
 LENGTH: 114
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-300-1551

Query Match 86.7%; Score 26; DB 10; Length 114;
 Best Local Similarity 80.0%; Pred. No. 3.6e+02; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSQCR 5
 ||:||
 Db 76 YSRCR 80

Db 103 FSQCR 107
 RESULT 8
 US-09-734-569-130
 Sequence 130; Application US/09734569
 Patent No. US20020064816A1
 GENERAL INFORMATION:
 APPLICANT: Lerchl, Jens
 APPLICANT: Renz, Andreas
 APPLICANT: Reindl, Andreas
 APPLICANT: Cirpus, Petra
 APPLICANT: Bischoff, Friedrich
 APPLICANT: Frank, Markus
 APPLICANT: Freund, Annette
 APPLICANT: Duwering, Elke
 APPLICANT: Schmidt, Ralf-Michael
 APPLICANT: Restl, Ralf
 TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved in the synthesis of carbohydrates
 FILE REFERENCE: BASF-NAE-133-NAE-99-US
 CURRENT APPLICATION NUMBER: US/09/734,569
 CURRENT FILING DATE: 2001-05-24
 PRIORITY APPLICATION NUMBER: US 60/171,101
 PRIOR FILING DATE: 1999-12-16
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: Patentin Ver. 2.1/wordperfect 6.1
 SEQ ID NO 130
 LENGTH: 199
 TYPE: PRT
 ORGANISM: Physcomitrella patens
 US-09-734-569-130

Query Match 86.7%; Score 26; DB 10; Length 199;
 Best Local Similarity 80.0%; Pred. No. 5.9e+02; Mismatches 0; Indels 1; Gaps 0;
 Matches 4; Conservative 0; Missmatches 1;
 Qy 1 YSQCR 5
 Db 56 YQQCR 60

RESULT 9
 US-09-841-132-20
 Sequence 20; Application US/09841132
 Patent No. US20020051848A1
 GENERAL INFORMATION:
 APPLICANT: Bhatia, Ajay
 APPLICANT: Shekly, Yasir A.W.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 FILE REFERENCE: 200121_469CB
 CURRENT APPLICATION NUMBER: US/09/841,132
 CURRENT FILING DATE: 2001-04-23
 NUMBER OF SEQ ID NOS: 599
 SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
 SEQ ID NO 20
 LENGTH: 216
 TYPE: PRT
 ORGANISM: Chlamydia trachomatis
 US-09-841-132-20

Query Match 86.7%; Score 26; DB 10; Length 216;
 Best Local Similarity 80.0%; Pred. No. 6.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Missmatches 0;
 Qy 1 YSQCR 5
 Db 102 YSKCR 106

Query Match 86.7%; Score 26; DB 10; Length 253;
 Best Local Similarity 80.0%; Pred. No. 7.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Missmatches 1;
 Qy 1 YSQCR 5
 Db 109 YQQCR 113

RESULT 10
 US-09-925-300-1601
 Sequence 5525; Application US/09738626
 Publication No. US20020197605A1
 GENERAL INFORMATION:
 APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOGUCHI, HIROSHI
 APPLICANT: ANDO, SEIKO
 APPLICANT: HAYASHI, MIKIRO
 APPLICANT: OCHIAI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOH, AKIHIRO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US/09/738,626
 CURRENT FILING DATE: 2000-12-18
 PRIORITY APPLICATION NUMBER: JP 99/377484
 PRIORITY FILING DATE: 1999-12-16
 PRIORITY APPLICATION NUMBER: JP 00/159162
 PRIORITY FILING DATE: 2000-04-07
 PRIORITY APPLICATION NUMBER: JP 00/280988
 PRIORITY FILING DATE: 2000-08-03
 SOFTWARE: Patentin ver. 3.0
 SEQ ID NO 5525
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-5525

Query Match 86.7%; Score 26; DB 9; Length 289;
 Best Local Similarity 80.0%; Pred. No. 8.2e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Missmatches 1;
 Qy 1 YSQCR 5
 Db 265 YQQCR 269

RESULT 12

US-09-962-276-2

Sequence 2, Application US/09962276

; Patent No. US200300215570A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001156DTV

CURRENT APPLICATION NUMBER: US/09/962,276

CURRENT FILING DATE: 2001-09-26

PRIORITY NUMBER: 60/210,458

PRIORITY FILING DATE: 2000-05-09

PRIORITY APPLICATION NUMBER: 09/799,345

PRIORITY FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 295

TYPE: PRT

ORGANISM: Human

US-09-962-276-2

Query Match

Best Local Similarity 86.7%; Score 26; DB 10; Length 295;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSQCR 5

Db 208 YKQCR 212

RESULT 13

US-10-007-521-10

Sequence 10, Application US/10007521

Publication No. US20030054539A1

GENERAL INFORMATION:

APPLICANT: Schultein, Martin

Andersen, Lene N.

Lassen, Soren F.

Kauppinen, Markus S.

Langbe, Lone

Nielsen, Ruby T.

Ihara, Michiko

Takagi, Shinobu

TITLE OF INVENTION: NO. US20030054539A1 Endoglucanases

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSE: NO. US20030054539A1 No. US20030054539A1disk of No. US200300545

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/007,521

FILING DATE: 10-DEC-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/651,136

FILING DATE: 21-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4366-200-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-857-0123

TELEFAX: 212-878-9855

SEQUENCE FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-007-521-10

Query Match

Best Local Similarity 86.7%; Score 26; DB 9; Length 349;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQCR 5

Db 339 YSQCC 343

RESULT 14

US-10-155-761-8811

Sequence 8811, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIRA, TADAKOHI

APPLICANT: SAKAKI, YOSHIOKI

APPLICANT: HATOTORI, MASAMURA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2003-05-29

PRIORITY NUMBER: JP 2001-204089

PRIORITY FILING DATE: 2001-05-30

PRIORITY APPLICATION NUMBER: JP 2001-272697

PRIORITY FILING DATE: 2001-06-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 8811

LENGTH: 356

TYPE: PRT

ORGANISM: Streptomyces avermitilis

US-10-156-761-8811

Query Match

Best Local Similarity 86.7%; Score 26; DB 9; Length 356;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSQCR 5

Db 101 YQCCR 105

RESULT 15

US-10-104-580-8

Sequence 8, Application US/10104580

Publication No. US20030033628A1

GENERAL INFORMATION:

APPLICANT: Straas, et al.

TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in

TITLE OF INVENTION: Poplar and other plant species.

FILE REFERENCE: 62486

CURRENT APPLICATION NUMBER: US/10/104,580

CURRENT FILING DATE: 2002-03-21

PRIORITY NUMBER: 09/410,464

PRIORITY FILING DATE: 1999-10-01

PRIORITY APPLICATION NUMBER: 09/287,700

PRIORITY FILING DATE: 1999-04-06

PRIORITY APPLICATION NUMBER: 60/080,851

PRIOR FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 8
LENGTH: 377
TYPE: PRT
ORGANISM: *Populus balsamifera* subsp. *trichocarpa*
US-10-104-S80-8

Query Match 86.7%; Score 26; DB 9; Length 377;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Index 0;
Gaps 0;
Qy 1 YSQCR 5
Db 233 YEQCR 237

Search completed: July 9, 2003, 12:17:58
Job time : 20.25 secs

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OM protein - protein search, using SW model
Run on: July 9, 2003, 12:00:11 ; Search time 143.25 Seconds
(without alignments), updates/sec 22.504 Million cell/sec

Title: US-09-851-058-2
Perfect score: 30
Sequence: 1 YSQCR 5

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : Pending Patents AA Main:*

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10: /cgn2_6/ptodata/1/paa/US086_COMB_pep: *
11: /cgn2_6/ptodata/1/paa/US087_COMB_pep: *
12: /cgn2_6/ptodata/1/paa/US088_COMB_pep: *
13: /cgn2_6/ptodata/1/paa/US089_COMB_pep: *
14: /cgn2_6/ptodata/1/paa/US090_COMB_pep: *
15: /cgn2_6/ptodata/1/paa/US091_COMB_pep: *
16: /cgn2_6/ptodata/1/paa/US092_COMB_pep: *
17: /cgn2_6/ptodata/1/paa/US093_COMB_pep: *
18: /cgn2_6/ptodata/1/paa/US094_COMB_pep: *
19: /cgn2_6/ptodata/1/paa/US095_COMB_pep: *
20: /cgn2_6/ptodata/1/paa/US096_COMB_pep: *
21: /cgn2_6/ptodata/1/paa/US097_COMB_pep: *
22: /cgn2_6/ptodata/1/paa/US098_COMB_pep: *
23: /cgn2_6/ptodata/1/paa/US099_COMB_pep: *
24: /cgn2_6/ptodata/1/paa/US100_COMB_pep: *
25: /cgn2_6/ptodata/1/paa/US101_COMB_pep: *
26: /cgn2_6/ptodata/1/paa/US102_COMB_pep: *
27: /cgn2_6/ptodata/1/paa/US60_COMBO.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
SUMMARIES				
1	30	100.0	35	27 US-60-136-244-154 Sequence 154, APP
2	30	100.0	54	27 US-60-142-896-1326 Sequence 1326, APP
3	30	100.0	54	27 US-60-143-992-1191 Sequence 1191, APP
4	30	100.0	61	20 US-60-617-681A-8383 Sequence 8383, APP
5	30	100.0	87	27 US-60-311-261-2772 Sequence 2772, APP
6	30	100.0	119	20 US-09-617-681A-8381 Sequence 8381, APP

RESULT 1
US-60-136-244-154
; Sequence 154, Application US/60136244
; GENERAL INFORMATION:
; APPLICANT: Kerlavage, Anthony
; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CL000019
; CURRENT APPLICATION NUMBER: US/60/136,244
; CURRENT FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: BlastSeq for Windows Version 3.0
; SEQ ID NO 154
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Drosophila
; US-60-136-244-154

Query Match Best Local Similarity 100.0%; Score 30; DB 27; Length 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 YSQCR 5
Db	14 YSQCR 18

RESULT 2
US-60-142-896-1326

SEQUENCE 1326, APPLICATION US/60142896
 GENERAL INFORMATION:
 APPLICANT: Kerlavage, Anthony
 TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
 FILE REFERENCE: CLO00052
 CURRENT APPLICATION NUMBER: US/60/142,896
 CURRENT FILING DATE: 1999-07-08
 NUMBER OF SEQ ID NOS: 1584
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1326
 LENGTH: 54

TYPE: PRT
 ORGANISM: Drosophila
 US-60-142-896-1326

Query Match Similarity 100.0%; Score 30; DB 27; Length 54;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 11 YSQCR 15

RESULT 3
 US-60-142-992-1191

Sequence 1191, Application US/60143992
 GENERAL INFORMATION:
 APPLICANT: Kerlavage, Anthony
 TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
 FILE REFERENCE: CLO00057
 CURRENT APPLICATION NUMBER: US/60/143,992
 CURRENT FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 1536
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1191
 LENGTH: 54

TYPE: PRT
 ORGANISM: Drosophila
 US-60-143-992-1191

Query Match Similarity 100.0%; Score 30; DB 27; Length 54;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOCH 5
 Db 11 YSOCH 15

RESULT 4
 US-60-142-8833

Sequence 8833, Application US/6017681A
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: CLO00058
 CURRENT APPLICATION NUMBER: US/09/617,681A
 CURRENT FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 9311
 SEQ ID NO 8833
 LENGTH: 61

TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE: misc_feature
 LOCATION: 1..61

OTHER INFORMATION: Drosophila

RESULT 5
 US-60-311-261-2772

Sequence 2772, Application US/60311261
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Zhilwei
 APPLICANT: Ma, Yunqiang
 TITLE OF INVENTION: Novel Nucleic Acids and Secreted Polypeptides
 FILE REFERENCE: 806
 CURRENT APPLICATION NUMBER: US/60/311,261
 CURRENT FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

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PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

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PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

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PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

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PRIOR APPLICATION NUMBER: US 09/491,404

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PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

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PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

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PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

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PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/577,409

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

RESULT 6
US-09-617-681A-8381
Sequence 8381; Application US/09617681A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1064P
CURRENT APPLICATION NUMBER: US/09/617,681A
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 9311
SEQ ID NO: 8381
LENGTH: 119
TYPE: PRT
ORGANISM: *Arabidopsis thaliana*
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..119
OTHER INFORMATION: Ceres Seq. ID 1439793
NAME/KEY: misc feature
LOCATION: 1..119
OTHER INFORMATION: Xaa is any amino acid
US-09-617-681A-8381

Query Match 100.0%; Score 30; DB 20; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 106 YSQCR 110

RESULT 7
US-60-140-956-2061
Sequence 2061; Application US/60140956
GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CIGO0041

CURRENT APPLICATION NUMBER: US/60/140,956
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 2638
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 2061
LENGTH: 132
TYPE: PRT
ORGANISM: *Drosophila*

US-60-140-956-2061

Query Match 100.0%; Score 30; DB 27; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 15 YSQCR 19

RESULT 8
US-60-142-896-1526
Sequence 1526; Application US/60142896
GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CIGO0052

CURRENT APPLICATION NUMBER: US/60/142,896
CURRENT FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 1584
SOFTWARE: FastSEQ for Windows Version 3.0

RESULT 9
PCT-US01-14827-10486
Sequence 10486; Application PC/TUS0114827
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 16102
SOFTWARE: Custom
SEQ ID NO: 10486
LENGTH: 214
TYPE: PRT
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (43)..(64)
OTHER INFORMATION: GTP/GCG GTP-BINDING PROTEIN FAMILY SIGNATURE domain
OTHER INFORMATION: Identified by eMATRIX, accession number PRO0326A, p-value=6.25
PCT-US01-14827-10486

Query Match 100.0%; Score 30; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 6 YSQCR 10

RESULT 10
US-10-027-150-22
Sequence 22; Application US/10027450
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO: 22
LENGTH: 243
TYPE: PRT

;

US-10-027-450-22

;

Query Match 100.0%; Score 30; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 68 YSQCR 72

RESULT 11

US-10-219-999-56114

;

Sequence 56114, Application US/10219999

;

GENERAL INFORMATION:

;

APPLICANT: Cao, Yongwei

;

APPLICANT: Edgeton, Michael D

;

APPLICANT: Hinkie, Gregory J.

;

APPLICANT: Kovacic, David K.

;

APPLICANT: Stein, Joshua

;

TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

;

FILE REFERENCE: 38-10/52767C

;

CURRENT APPLICATION NUMBER: US/10/219,999

;

CURRENT FILING DATE: 2002-08-15

;

PRIOR APPLICATION NUMBER: US 60/324,109

;

PRIOR FILING DATE: 2001-09-21

;

APPLICATION NUMBER: US 60/312,544

;

PRIOR FILING DATE: 2001-08-15

;

NUMBER OF SEQ ID NOS: 63520

;

SEQ ID NO 19630

;

LENGTH: 371

;

TYPE: PRT

;

ORGANISM: Pseudomonas aeruginosa

;

US-09-252-991A-19630

;

Query Match 100.0%; Score 30; DB 26; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 32 YSQCR 36

RESULT 12

US-09-708-427-17469

;

Sequence 17468, Application US/09708427

;

GENERAL INFORMATION:

;

APPLICANT: N ALEKANDROV et al.

;

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

;

FILE REFERENCE: 2750-1243P

;

CURRENT APPLICATION NUMBER: US/09/708,427

;

CURRENT FILING DATE: 2000-11-09

;

NUMBER OF SEQ ID NOS: 85364

;

SOFTWARE: Patentin version 3.1

;

SEQ ID NO 17467

;

LENGTH: 377

;

TYPE: PRT

;

ORGANISM: Arabidopsis thaliana

;

FEATURE: NAME/KEY: misc_feature

;

LOCATION: 1..377

;

OTHER INFORMATION: xaa is any amino acid

;

NAME/KEY: misc_feature

;

LOCATION: 1..377

;

OTHER INFORMATION: Ceres Seq. ID 1832394

;

US-09-708-427-17467

;

Query Match 100.0%; Score 30; DB 21; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 191 YSQCR 195

RESULT 15

US-09-708-427-17468

;

Query Match 100.0%; score 30; DB 21; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 368;

RESULT 15

US-09-708-427-17466

; Sequence 17466 Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 83364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17466
; LENGTH: 516

; TYPE: PRY
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY misc-feature
; LOCATION: 1..516
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY misc-feature
; LOCATION: 1..516
; OTHER INFORMATION: Ceres Seq .ID 1832393
; US-09-708-427-17466

Query Match 100.0%; Score 30; DB 21; Length 516;
Best local Similarity 100.0%; Pred. No. 1 5e+03; Mismatches 0;
Matches 5; Conservative 0; Indels 0; Gaps 0;
Qy 1 YSQCR 5
Db 330 YSQCR 334
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Search completed: July 9, 2003, 12:13:17
Job time : 165.25 secs

This Page Block (Supro)

GenCore version 5.1.6
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Run on: July 9, 2003, 12:00:51 ; Search time 47.25 Seconds
(without alignments)
27.740 Million cell updates/sec

Title: US-09-851-058-2
Perfect score: 30 1 YSQR 5

Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1221054 seqs, 262139423 residues

Total number of hits satisfying chosen parameters: 1221054

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New.*

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2: /cgn2_6/prodata/1/paa/PCT_NEW_COMB_pep4:*

3: /cgn2_6/prodata/1/paa/US06_NEW_COMB_pep:*

4: /cgn2_6/prodata/1/paa/US06_NEAL_COMB_pep4:*

5: /cgn2_6/prodata/1/paa/US07_NEW_COMB_pep:*

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8: /cgn2_6/prodata/1/paa/US08_NEW_COMB_pep4:*

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12: /cgn2_6/prodata/1/paa/US10_NEAL_COMB_pep4:*

13: /cgn2_6/prodata/1/paa/US60_NEW_COMB_pep:*

14: /cgn2_6/prodata/1/paa/US60_NEAL_COMB_pep4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	30	100 0	5	2	PCT-US02-14369-2	Sequence 2, Appli
2	30	100 0	5	10	US-09-851-058-2	Sequence 2, Appli
3	30	100 0	60	12	US-10-424-599-15972	Sequence 145972
4	30	100 0	87	12	US-10-219-382-2172	Sequence 2772, Ap
5	30	100 0	87	12	US-10-219-382A-2772	Sequence 2772, Ap
6	30	100 0	108	12	US-10-424-599-29646	Sequence 229645,
7	30	100 0	280	12	US-10-425-114-63966	Sequence 64966, A
8	30	100 0	332	12	US-10-437-963-13488	Sequence 173488,
9	30	100 0	371	12	US-10-366-683-1630	Sequence 19630, A
10	30	100 0	371	12	US-10-419-128-1630	Sequence 19630, A
11	30	100 0	729	12	US-10-369-493-6201	Sequence 6201, Ap
12	27	90 0	5	10	US-09-851-058-3	Sequence 3, Appli
13	27	90 0	5	10	US-09-851-058-3	Sequence 3, Appli
14	27	90 0	38	12	US-10-424-599-17300	Sequence 157300,
15	27	90 0	83	12	US-10-424-599-165725	Sequence 165725
16	27	90 0	85	12	US-10-424-599-160856	Sequence 180856,
17	27	90 0	109	12	US-10-424-599-171831	Sequence 171831,
18	27	90 0	124	12	US-09-864-408A-292	Sequence 292, Ap
19	27	90 0	124	12	US-10-218-140-574	Sequence 574, Ap

ALIGNMENTS

RESULT 1
PCT-US02-14369-2

; Sequence 2, Application PC/TUS0214369
; GENERAL INFORMATION:
; APPLICANT: Parker, Kenneth
; APPLICANT: Nadler, Timothy
; APPLICANT: Huang, Yulin
; APPLICANT: Abersold, Rudolf
; APPLICANT: Smolka, Marcus
; TITLE OF INVENTION: Process for Analyzing Protein
; FILE REFERENCE: SIP-172
; CURRENT APPLICATION NUMBER: PCT/US02/14369
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptides
PCT-US02-14369-2

Query Match Score 100.0%; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e+06
Matches 5; Conservative 0; Mismatches 0

QY 1 YSQR 5

Db 1 YSQR 5

RESULT 2
US-09-851-058-2

; Sequence 2, Application US/09851058
; GENERAL INFORMATION:
; APPLICANT: Parker, Kenneth
; APPLICANT: Nadler, Timothy
; APPLICANT: Vella, George
; APPLICANT: Huang, Yulin
; APPLICANT: Abersold, Rudolf

PRIOR FILING DATE: 2000-05-19
 REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 2818
 SOFTWARE: PL_FLI_genes Version 5.0
 SEQ ID NO: 2772
 LENGTH: 87
 TYPE: PRT
 FEATURE:
 ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 LOCATION: (1)..(87)
 OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the Table 8 as set for
 US-10-219-382A-2772

Qy	1 YSQCR 5	Score: 100.0%	DB: 12	Length: 87
Db	58 YSQCR 62	Pred. No.: 1.2e+02;		
		Mismatches: 5;	Conservative: 0;	Indels: 0; Gaps: 0;

RESULT 6
 US-10-424-599-229646
 Sequence 229646, Application US/10424599
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovacic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 Title of Invention: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10-424, 599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285664
 SEQ ID NO: 229646
 LENGTH: 108
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(108)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_49395C.1.pep
 US-10-424-599-229646

Qy	Query Match: 100.0% Score: 30; DB: 12; Length: 108; Best Local Similarity: 100.0%; Pred. No.: 1.4e+02; Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
----	--

RESULT 7
 US-10-425-114-64966
 Sequence 64966, Application US/10425114
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovacic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 Title of Invention: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5331)B
 CURRENT APPLICATION NUMBER: US/10-425, 114
 CURRENT FILING DATE: 2003-04-28

Qy	Query Match: 100.0% Score: 30; DB: 12; Length: 108; Best Local Similarity: 100.0%; Pred. No.: 1.4e+02; Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
----	--

RESULT 8
 US-10-437-963-17488
 Sequence 17488, Application US/10437963
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 Title of Invention: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5321)B
 CURRENT APPLICATION NUMBER: US/10-437, 963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO: 173488
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_71520C.1.pep
 US-10-437-963-173488

Qy	Query Match: 100.0% Score: 30; DB: 12; Length: 332; Best Local Similarity: 100.0%; Pred. No.: 3e+02; Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
----	--

RESULT 9
 US-10-366-683-19630
 Sequence 19630, Application US/10366683
 GENERAL INFORMATION:
 APPLICANT: Rubenfield, Marc J.
 APPLICANT: Nolling, Jork
 APPLICANT: Deloughery, Craig
 APPLICANT: Bush, David
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 Title of Invention: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: PATH03-04
 CURRENT APPLICATION NUMBER: US/10-366, 983
 CURRENT FILING DATE: 2003-02-13
 PRIOR APPLICATION NUMBER: 09/2322, 991
 PRIOR FILING DATE: 1999-02-18
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 19630
 LENGTH: 371
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

US-10-366-683-19630

Query Match 100.0%; Score 30; DB 12; Length 371;

Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 115 YSQCR 119

RESULT 10

US-10-419-128-19630
Sequence 19630, Application US/10419128

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/10/19,128

CURRENT FILING DATE: 2003-04-21

PRIOR APPLICATION NUMBER: US/09/252,991

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19630

LENGTH: 371

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-10-419-128-19630

Query Match 100.0%; Score 30; DB 12; Length 371;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 115 YSQCR 119

RESULT 11

US-10-369-493-6201

Sequence 6201, Application US/10369493

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(5202)B

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6201

LENGTH: 729

TYPE: PRT

ORGANISM: Caenorhabditis elegans

US-10-369-493-6201

Query Match 100.0%; Score 30; DB 12; Length 729;

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 536 YSQCR 540

RESULT 12

PCT-US02/14369-3

SEQUENCE 3, Application PC/PCTUS02/14369

GENERAL INFORMATION:

APPLICANT: Parker, Kenneth

APPLICANT: Nadler, Timothy

APPLICANT: Veila, George

APPLICANT: Huang, Yulin

APPLICANT: Abersold, Rudolf

APPLICANT: Smolka, Marcus

TITLE OF INVENTION: Process for Analyzing Protein Samples

FILE REFERENCE: SYP-172

CURRENT APPLICATION NUMBER: PCT/US02/14369

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 3

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic peptides

PCT-US02/14369-3

Query Match 90.0%; Score 27; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 1.1e+06; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 1 YTQCR 5

RESULT 13

US-09-851-058-3

Sequence 3, Application US/09851058

GENERAL INFORMATION:

APPLICANT: Parker, Kenneth

APPLICANT: Nadler, Timothy

APPLICANT: Veila, George

APPLICANT: Huang, Yulin

APPLICANT: Abersold, Rudolf

APPLICANT: Smolka, Marcus

TITLE OF INVENTION: Process for Analyzing Protein Samples

FILE REFERENCE: SYP-172

CURRENT APPLICATION NUMBER: US/09/851,058

CURRENT FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic peptides

US-09-851-058-3

Query Match 90.0%; Score 27; DB 10; Length 5;

Best Local Similarity 80.0%; Pred. No. 1.1e+06; Mismatches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 1 YTQCR 5

RESULT 14

US-10-424-599-157300

Sequence 157300, Application US/10424599

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovacic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 SEQ ID NO: 157300
 LENGTH: 38
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_113062C.1.pep
 US-10-424-599-157300

Query Match	Best Local Similarity	Score	Pred. No.	Length
Matches	80.0%	27	2.9e+02	38
Qy	1 YSOCR 5			
Db	28 YAOCR 32			

RESULT 15
 US-10-424-599-165725
 ; Sequence 165725; Application US/10424599
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovacic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO: 165725
 LENGTH: 83
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_120665C.1.pep
 US-10-424-599-165725

Query Match	Best Local Similarity	Score	DB	Length
Matches	80.0%	27	12	83
Qy	1 YSOCR 5			
Db	16 YSECRR 20			

Search completed: July 9, 2003, 12:16:32
 Job time : 49.25 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:58:06 ; Search time 9.25 Seconds
(without alignments)

Title: US-09-851-058-2
Perfect score: 30
Sequence: 1 YSQCR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*

1: Pirl1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
T20781
hypothetical protein F11D11.8 - *Caenorhabditis elegans*

C; Species: *Caenorhabditis elegans*
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C; Accession: T20781
R; Mortimore, B.; Basham, V.
submitted to the EMBL Data Library, November 1996

A; Reference number: Z19123
A; Accession: T20781

A; Status: preliminary; translated from GB/EMBL/DDBBJ

A; Molecule type: DNA

A; Residues: 1-221 <HL>

A; Cross-references: EMBL:Z81500; PIDN:GAB04099.1; GSPDB:GN00023; CESP:F11D11.8

A; Experimental source: clone F11D11

C; Genetics:

A; Gene: CESP:F11D11.8

A; Map position: 5

A; Introns: 69/3

Result No.	Score	Query Match Length	DB ID	Description
1	30	100.0	T20781	hypothetical prote
2	30	100.0	341 2	conserved hypothet
3	30	100.0	516 2	probable nucleosid
4	30	100.0	729 2	hypothetical prote
5	27	90.0	78 2	hypothetical prote
6	27	90.0	155 2	eosinophil-associa
7	27	90.0	156 2	chorismate mutase
8	27	90.0	315 2	transcription regu
9	27	90.0	F82135	hypothetical prote
10	27	90.0	378 2	eosinophil-associa
11	27	90.0	451 2	hypothetical prote
12	27	90.0	501 2	hypothetical prote
13	27	90.0	692 2	A-kinase anchor pr
14	27	90.0	860 2	hypothetical prote
15	27	90.0	1171 2	hypothetical prote
16	27	90.0	1691 1	genomic polyprotein
17	27	90.0	1693 1	genomic polyprotein
18	26	86.7	121 2	hypothetical prote
19	26	86.7	127 2	hypothetical prote
20	26	86.7	185 1	ribosomal protein
21	26	86.7	T03233	probable ribosomal
22	26	86.7	188 2	probable CDP-alcoh
23	26	86.7	E1157	hypothetical prote
24	26	86.7	AG2434	probable DNA-bind
25	26	86.7	T16049	splicing factor SR
26	26	86.7	86155	probable membrane
27	26	86.7	867	probable membrane
28	26	86.7	259 2	hypothetical prote
29	26	86.7	S27955	probable transcript
30	26	86.7	298 2	2-phosphoglycerate
31	26	86.7	D83319	probable transcrip
32	26	86.7	304 2	LFLY floral meriste
33	26	86.7	S41582	flo protein homolo

Result No.	Score	Query Match Length	DB ID	Description
1	30	100.0	T20781	hypothetical protein F11D11.8 - <i>Caenorhabditis elegans</i>
2	30	100.0	341 2	C; Species: <i>Caenorhabditis elegans</i>
3	30	100.0	516 2	C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
4	30	100.0	729 2	C; Accession: T20781
5	27	90.0	78 2	R; Mortimore, B.; Basham, V. submitted to the EMBL Data Library, November 1996
6	27	90.0	155 2	A; Reference number: Z19123
7	27	90.0	156 2	A; Accession: T20781
8	27	90.0	315 2	A; Status: preliminary; translated from GB/EMBL/DDBBJ
9	27	90.0	F82135	A; Molecule type: DNA
10	27	90.0	378 2	A; Residues: 1-221 <HL>
11	27	90.0	451 2	A; Cross-references: EMBL:Z81500; PIDN:GAB04099.1; GSPDB:GN00023; CESP:F11D11.8
12	27	90.0	501 2	A; Experimental source: clone F11D11
13	27	90.0	692 2	C; Genetics:
14	27	90.0	860 2	A; Gene: CESP:F11D11.8
15	27	90.0	1171 2	A; Map position: 5
16	27	90.0	1691 1	A; Introns: 69/3
17	27	90.0	1693 1	RESULT 2
18	26	86.7	121 2	B82790 conserved hypothetical protein XF0556 [imported] - <i>Xylella fastidiosa</i> (strain 9a5c)
19	26	86.7	127 2	C; Species: <i>Xylella fastidiosa</i>
20	26	86.7	185 1	C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
21	26	86.7	T03233	C; Accession: B82790
22	26	86.7	188 2	R; Anonymous: The <i>Xylella fastidiosa</i> Consortium of the Organization for Nucleotide Seq
23	26	86.7	E1157	Nature 406, 151-157, 2000
24	26	86.7	AG2434	A; Title: The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .
25	26	86.7	T16049	A; Reference number: A82515; PMID:1036517; PMID:1091047
26	26	86.7	86155	A; Note: for a complete list of authors see reference number A59328 below
27	26	86.7	867	A; Accession: B82790
28	26	86.7	259 2	A; Status: preliminary
29	26	86.7	S27955	A; Molecule type: DNA
30	26	86.7	298 2	A; Residues: 1-341 <SIM>
31	26	86.7	D83319	A; Cross-references: GB:AE003903; GB:AE003849; NID:9105416; PIDN:AAFS3366.1; GSPDB:GN
32	26	86.7	304 2	A; Experimental source: strain 9a5c
33	26	86.7	S41582	R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acebedo, M.; Alvaranga, R.
34	26	86.7	221 2	Briones, M.R.P.; Bueno, M.R.P.; Camargo, L.E.A.; Carrero, D.M.; Carrer
35	26	86.7	559075	as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
36	26	86.7	T13162	submitted to GenBank, June 2000
37	26	86.7	867	A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
38	26	86.7	259 2	J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramane, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.; Martins, E.N.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rose, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santeilli, R.V.; Sawasaki, M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsunoi, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; Reference number: A59328; A:Contents: annotation; C:Genetics: A:Gene: XF0556

RESULT 3

Query Match	100.0%	Score 30;	DB 2;	Length 341;
Best Local Similarity	100.0%	Pred. No.	59;	
Matches	5;	Conservative	0;	Mismatches
OY	1	YSOCR 5		
Db	34	YSOCR 38		

|||||

probable nucleoside triphosphatase [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Accession: GB4442 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

RiLin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; eubs, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Selzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A64420; MUID:20083487; PMID:10517197

A:Accession: G64442

A:Status: preliminary

A:Residues: 1-516 <STO>

A:Cross-references: GB:AE002093; NID:93461821; PIDN:AC32915.1; GSPDB:GN00139

A:Genetics:

A:Map position: 2

Query Match

100.0%	Score 30;	DB 2;	Length 516;	
Best Local Similarity	100.0%	Pred. No.	83;	
Matches	5;	Conservative	0;	Mismatches
OY	1	YSOCR 5		
Db	330	YSOCR 34		

|||||

RESULT 4

T23474	hypothetical protein K08E7_7 - <i>Caenorhabditis elegans</i>
C:Species: <i>Caenorhabditis elegans</i>	
C:Accession: T23474 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999	
R:Syme, R.	
submitted to the EMBL Data Library, July 1996	
A:Reference number: Z19745	
A:Accession: T23474	
A:Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-729 <WIL>	
A:Cross-references: EMBL:Z77666; PIDN:CAB01230.1; GSPDB:GN00022; CESP:K08E7_7	
A:Experimental source: clone K08E7	
C:Genetics:	
A:Gene: CESP:K08E7_7	
A:Map position: 4	
A:Introns: 33/2; 292/2; 405/3; 555/3; 665/3; 686/3	

Query Match

100.0%	Score 30;	DB 2;	Length 729;	
Best Local Similarity	100.0%	Pred. No.	1.1e+02;	
Matches	5;	Conservative	0;	Mismatches
OY	1	YSOCR 5		
Db	115	YSOCR 119		

|||||

RESULT 5

T17891	hypothetical protein a388R - <i>Chlorella virus PBCV-1</i>
C:Species: <i>Chlorella virus PBCV-1</i>	
C:Accession: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999	
R:Graves, M.V.; Van Etten, J.L.	
submitted to the EMBL Data Library, May 1999	
A:Reference number: Z18806	
A:Accession: T17891	
A:Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-78 <GRA>	
A:Cross-references: EMBL:U42580; NID:94028896; PIDN: AAC96756.1	
A:Experimental source: specific host <i>Chlorella</i> strain NC64A	
C:Genetics:	
A:Note: a388R	

Query Match

90.0%	Score 27;	DB 2;	Length 78;	
Best Local Similarity	80.0%	Pred. No.	78;	
Matches	4;	Conservative	1;	Mismatches
OY	1	YSOCR 5		
Db	27	YSOCR 31		

|||||

RESULT 6

JC6159	eosinophil-associated ribonuclease (EC 3.1.1.-) 1 precursor - mouse
C:Species: <i>Mus musculus</i> (house mouse)	
C:Accession: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999	
R:Larson, K.A.; Olson, E.V.; Madden, B.J.; Gleich, G.J.; Lee, N.A.; Lee, J.J.	
Proc. Natl. Acad. Sci. U.S.A. 93, 12370-12375, 1996	
A:Title: Two highly homologous ribonuclease genes expressed in mouse eosinophils Iden	
A:Reference number: JC6159; MUID:97057249; PMID:8901588	
A:Accession: JC6159	
A:Molecule type: mRNA	
A:Residues: 1-155 <LAR1>	
A:Cross-references: GB:U70232; NID:91695898; PIDN:AAB37786.1; PID:91695899	
A:Accession: PC6041	
A:Molecule type: protein	
A:Residues: 52-75,137-149 <LAR2>	
A:Experimental source: bone marrow	
C:Genetics:	
A:Gene: near-1	
C:Superfamily: pancreatic ribonuclease	
C:Keywords: bone; disulfide bond; glycoprotein; hydrolase; RNA binding	
F:1-27-domain: signal sequence #status predicted <SIG>	
F:28-155/Product: eosinophil-associated ribonuclease 1 #status predicted <MAT>	
F:38,62,150/Active site: His, Lys, His #status predicted	
F:41,95,107,114/Binding site: carbohydrate (Asn) (covalent) #status predicted	
F:47-106,61-118,79-133,86-94/Disulfide bonds: #status predicted	

Query Match

90.0%	Score 27;	DB 2;	Length 155;	
Best Local Similarity	80.0%	Pred. No.	1.3e+02;	
Matches	4;	Conservative	1;	Mismatches
OY	1	YSOCR 5		
Db	115	YSOCR 119		

|||||

RESULT 7

JC6160	eosinophil-associated ribonuclease (EC 3.1.1.-) 2 precursor - mouse
--------	---

C;Species: *Mus musculus* (house mouse)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C;Accession: JG6150; PIDN:PC6042
R;Larson, K.A.; Olson, E.V.; Madden, B.J.; Gleich, G.J.; Lee, N.A.; Lee, J.J.
Proc. Natl. Acad. Sci. U.S.A. 93, 12370-12375, 1996
A;Title: Two highly homologous ribonuclease genes expressed in mouse eosinophils identified
A;Reference number: JG6159; MUID:97057249; PMID:8901588
A;Accession: JG6160
A;Molecule type: mRNA
A;Residues: 1-156 <LAR1>
A;Cross-references: GB:U72031; NID:91695896; PIDN:AAB37785.1; PID:91695897
A;Experimental source: bone marrow
A;Accession: PC6042
A;Gene: near-2
A;Molecule type: protein
A;Residues: 52-77;138-150 <LAR2>
C;Genetics:
C;Superfamily: pancreatic ribonuclease
C;Keywords: bone; disulfide bond; glycoprotein; hydrolase; RNA binding
F;1-27/Domain: signal sequence #status predicted <SG>
F;28-155/Product: eosinophil-associated ribonuclease 2 #status predicted <MAT>
F;38-62,151/Active site: His, Lys; His #status predicted
F;47-106,61-119,79-114,86-94/disulfide bonds: #status predicted
F;89,96,107/Binding site: carbohydrate (asn) (covalent) #status predicted

RESULT 8

Query Match 90.0%; Score 27; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 1; MisMatches 0;

Oy 1 YSQCR 5
Db 116 YTQCR 120

RESULT 9

Query Match 90.0%; Score 27; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 1.3e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 1; MisMatches 0;

Oy 1 YSQCR 5
Db 116 YTQCR 120

RESULT 10

B85059
hypothetical protein At4g04690 [imported] - *Arabidopsis thaliana* (mouse-ear cress)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: B85059
R;anonymous, The European Union *Arabidopsis* Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85059
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: GB:NC_001268; NID:9726727; PIDN:CAB80834.1; GSPDB:GN00140
C;Genetics:
A;Gene: At4g04690
A;Map position: 4

RESULT 11

Query Match 90.0%; Score 27; DB 2; Length 378;
Best Local Similarity 80.0%; Pred. No. 2.7e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 1; MisMatches 0;

Oy 1 YSQCR 5
Db 194 YTQCR 198

RESULT 12

A70539
hypothetical protein Rv1128c - *Mycobacterium tuberculosis*
C;Species: *Mycobacterium tuberculosis*
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70539
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, F.; Connor, R.; Davies, R.; Devlin, K.; Feilwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajendram, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70539
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-451 <COL>
A;Cross-references: GB:G95585; GB:ALU123456; NID:93261787; PIDN:CAB09039.1; PID:921172
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1128c

C;Superfamily: Mycobacterium tuberculosis hypothetical protein Ru1945

Query Match 90.0%; Score 27; DB 2; Length 451;
Best Local Similarity 80.0%; Pred. No. 3.1e+02; 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 383 YACQR 387

RESULT 12

A70534 hypothetical protein Ru0654 - Mycobacterium tuberculosis (strain H37RV)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: A70534

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; NID:9295987; PMID:9634230

A;Accession: A70534

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-501 <CDS>

A;Cross-references: GB:95972; GB:AL123456; NID:9261790; PIDN:CA09380.1; PID:e319166;

A;Experimental source: strain H37RV

C;Genetics: Gene: Ru0654

Query Match 90.0%; Score 27; DB 2; Length 501;

Best Local Similarity 80.0%; Pred. No. 3.4e+02; 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 319 YSECR 323

RESULT 13

T13161 *A*-kinase anchor protein 95 - human

N;Alternate names: Protein DKFZp586B1222.1

C;Species: *Homo sapiens* (man)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13161; T08786

R;Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Viswanathan, V.; Burkhart-Schultz, K.; Dangaran, L.; Erter, A.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, J.; Quan, G.; Krommiller, B.; Arellano, A.; Saunders, C.; Ow, D.; Nolan, M.; Trong, S.

submitted to the EMBL Data Library, October 1998

A;Authors: Kobayashi, A.; Olsen, A.S.; Carano, A.V.

A;Description: Sequence analysis of a 1.5 Mb OLFR-rich region in 19p13.1.

A;Reference number: Z17617

A;Accession: T13161

A;Status: translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: J-692 <LAM>

A;Cross-references: EMBL:AC005785; NID:93702290; PID:93702291; PIDN: AAC62838.1

A;Experimental source: adult uterus; clone DKFZp586B1222

C;Genetics: Gene: DKFZp586B1222.1

A;Map position: 19: 201/ 31/1; 124/2; 287/3; 331/1; 346/3; 358/1; 387/2; 434/3; 456/1; 509/

RESULT 14

T15778 hypothetical protein C35B8.2 - *Cenorhabditis elegans*

C;Species: *Cenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000

C;Accession: T15778

R;Leimbach, D.

submitted to the EMBL Data Library, March 1995

A;Description: The sequence of *C. elegans* cosmid C35B8.

A;Reference number: 218401

A;Accession: T15778

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-860 <LEI>

A;Cross-references: EMBL:U23520; NID:9746532; PID:9746534;

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP-C35B8.2

A;Intons: 37/2; 67/3; 126/2; 173/2; 200/3; 304/2; 372/3; 565/2; 615/1; 677/3; 714/2;

C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-bindin

Query Match 90.0%; Score 27; DB 2; Length 860;

Best Local Similarity 80.0%; Pred. No. 5.2e+02; 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 853 YSQCK 857

RESULT 15

T12956 hypothetical protein T6H20_50 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999

C;Accession: T12956

R;Choisne, N.; Robert, C.; Brottier, P.; Wincier, P.; Cattolico, L.; Artiguena, F.;

submitted to the Protein Sequence Database, July 1999

A;Reference number: 217586

A;Accession: T12956

A;Molecule type: DNA

A;Residues: 1-171 <CHO>

A;Cross-references: EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20_50

A;Experimental source: cultivar Columbia; BAC clone T6H20

C;Genetics:

A;Gene: ATSP:T6H20_50

A;Map position: 3: 780/1; 857/3; 881/3; 932/3; 987/2; 1036/3; 1077/3; 1107/1

Query Match 90.0%; Score 27; DB 2; Length 1171;

Best Local Similarity 80.0%; Pred. No. 6.4e+02; 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
Db 580 YACQR 584

Search completed: July 9, 2003, 12:02:45

Job time: 11.25 secs

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Gencore version 5.1.6									
OM protein - protein search, using SW model									
Run on:	July 9, 2003, 11:55:50 ;	search time	7.75 seconds						
Sequence:	US-09-851-058-2	(without alignments)							
Scoring table:	BLOSUM62	26.759 Million cell updates/sec							
Perfect score:	30	Score:	1 YSOQR 5						
Searched:	112892 seqs, 41476328 residues								
Total number of hits satisfying chosen parameters:	112892								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing:	Minimum Match 0%								
	Maximum Match 100%								
Listing first 45 summaries									
database :	Swissprot_40_*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	30	100.0	210	1 PSBP_PORPU	P50277 porphyra pu	PSBP_PORPU	STANDARD;	PRT;	210 AA.
2	30	100.0	729	1 CUL6_CAEEL	Q21146 caenorhabdi	ID	P50272; STANDARD;		
3	27	90.0	155	1 ECPL_MOUSE	P97426 mus musculu	DT	01-OCT-1995 (Rel. 34, Created)		
4	27	90.0	155	1 ECP2_RAT	P77079 ratmus norv	DT	01-OCT-1995 (Rel. 34, Last sequence update)		
5	27	90.0	156	1 ECP2_MOUSE	P97425 mus musculu	DT	15-JUN-2002 (Rel. 41, Last annotation update)		
6	27	90.0	156	1 ECP3_MOUSE	Q35790 mus musculu	DE	Putative polysaccharide binding protein precursor,		
7	27	90.0	451	1 YB28_MICTU	O06580 mycobacteri	OS	porphyra purpurea.		
8	27	90.0	692	1 AKAB_HUMAN	O43823 homo sapien	OC	Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.		
9	27	90.0	1691	1 POIN_HEVME	Q03945 hepatitis e	OX	NCBI_TaxID:2787;		
10	27	90.0	1693	1 POLN_HEVBU	P29324 hepatitis e	RN	[1]		
11	27	90.0	1693	1 POLN_HEVMY	Q046310 hepatitis e	RC	SEQUENCE FROM N. A.		
12	27	90.0	1693	1 POLN_HEVPA	P33324 hepatitis e	RA	STRAIN:Avonport;		
13	26	86.7	185	1 RM16_MAIZE	P27927 zea mays (m	RL	deR Meer J.P., Reith M.E.; Liu Q.,		
14	26	86.7	185	1 RML6_ORYSA	P46801 oryza sativ	DR	Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.		
15	26	86.7	188	1 Y460_PYRHO	O58215 pyrococcus	DR	-1 SIMILARITY: CONTAINS 4 FUNGAL-TYPE CELLULOSE-BINDING DOMAINS (CBD).		
16	26	86.7	221	1 SFR9_HUMAN	Q13242 homo sapien	DR	CC		
17	26	86.7	298	1 Y33K_HUMAN	Q04323 homo sapien	DR	This SWISS-PROT entry is copyright. It is produced through a collaboration		
18	26	86.7	326	1 YDCK_ECOLI	P76100 escherichia	DR	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
19	26	86.7	359	1 FLL_EUCLG	O64953 eucalyptus	DR	the European Bioinformatics Institute. There are no restrictions on its		
20	26	86.7	377	1 FLLH_POPTR	O040564 populus tri	DR	use by non profit institutions as long as its content is in no way		
21	26	86.7	388	1 GUN3_HUMAN	O12624 humicola in	DR	modified and this statement is not removed. Usage by and for commercial		
22	26	86.7	389	1 FLF_ORYSA	O24175 oryza sativ	DR	entities requires a license agreement (see http://www.isb-sib.ch/announce/)		
23	26	86.7	395	1 UNI_PEA	O48559 pisiun sativ	DR	or send an email to license@isb-sib.ch).		
24	26	86.7	396	1 FLO_ANIMA	P23915 antirrhinum	FT			
25	26	86.7	412	1 ALF_PETHY	O22621 petunia hyb	FT			
26	26	86.7	413	1 FLL_TOBAC	Q40504 nicotiana t	FT			
27	26	86.7	415	1 BOFH_BRASS	O05536 brassica ol	FT			
28	26	86.7	416	1 FL2_TOBAC	O440505 nicotiana t	FT			
29	26	86.7	420	1 CRF1_CHICK	O90812 gallus gall	FT			
30	26	86.7	424	1 LFY_ARATH	O00958 arabidopsis	FT			
31	26	86.7	462	1 GUNB_FUSOX	P46236 fusarium ox	FT			
32	26	86.7	514	1 GUXC_FUSOX	P46238 fusarium ox	FT			
33	26	86.7	518	1 ORC2_XENLA	O91628 xenopus lae	FT			
RESULT 2									
Matches	5	Conservative	100.0%	O	0; Mismatches	0;	Indels	0;	Gaps 0;
	1 YSOQR 5								
Db	54	YSOQR 58							
ALIGNMENTS									
ALIGNS									
GCR_PIG	704	1 TRPL_PIG	771	1 GCR_CAVPO	86.7	ENV_BAEVM	34	baboon endo	P10259
VGL_HSVE	575	1 VGL_HSVE	86.7	1 CYAL_DROME	86.7	bovine hepc	35	drosophila	P12870
ORC2_MOUSE	576	1 ORC2_MOUSE	86.7	1 PON_RRN	86.7	mus musculu	36	ross river	P13887
Q13416_HUMAN	577	1 Q13416_HUMAN	86.7	1 PKSM_BACSU	86.7	homo sapien	37	bacillus su	P04872
Opnlu3_SUSCROFA	578	1 Opnlu3_SUSCROFA	86.7	1 YIM8_BPPH1	83.3	sus scrofa	38	bacterioph	P10431
P49115_CAVIA	579	1 P49115_CAVIA	86.7	1 P14915_cavia porce	83.3	cavia porce	39	endo	P12870
P14915_cavia	580	1 P14915_cavia	86.7	1 P14915_cavia porce	83.3	endo	40	drosophila	P12870
P14915_cavia	581	1 P14915_cavia	86.7	1 P14915_cavia porce	83.3	drosophila	41	endo	P12870
P14915_cavia	582	1 P14915_cavia	86.7	1 P14915_cavia porce	83.3	endo	42	endo	P12870
P14915_cavia	583	1 P14915_cavia	86.7	1 P14915_cavia porce	83.3	endo	43	endo	P12870
P14915_cavia	584	1 P14915_cavia	86.7	1 P14915_cavia porce	83.3	endo	44	endo	P12870

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cull-6 protein.
 GN Cull-6 OR KOBET-7.
 OS Caenorhabditis elegans
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderaeinae; Caenorhabditis.
 OC NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol NZ.
 RA Smyre R;
 RL Submitted (JUL-1996) to the EMBL/Genbank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CULLIN FAMILY.
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 DR EMBL; U77032; AAB37786.1;
 DR HSSP; P00656; 2RNS.
 DR MGD; MGI:10801; Earl.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINS; PRO704; RIBONUCLEASE.
 DR ProDom; PD000335; RNase; 1.
 DR SMART; SM00932; RNASE_P.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Pfam; PF00074; rnaseA; 1.
 DR HYDROLASE; NUCLEASE; Endonuclease; Eosinophil; Toxin; Glycoprotein;
 KW Signal.
 FT SIGNAL 1
 FT CHAIN 26 155
 FT ACT-SITE 38 38
 FT ACT-SITE 62 62
 FT ACT-SITE 150 150
 FT DISULFID 47 106
 FT DISULFID 61 118
 FT DISULFID 79 133
 FT DISULFID 86 94
 FT CARBOHYD 41 41
 FT CARBOHYD 96 96
 FT CARBOHYD 107 107
 FT CARBOHYD 114 114
 SQ SEQUENCE 155 AA; 17296 MW; F6264E7A3B20D87 CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 729;
 Best Local Similarity 90.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSQCR 5
 YSQCR 5
 Db 536 YSQCR 540

RESULT 3
 ECPL_MOUSE STANDARD: PRT; 155 AA.
 ID ECPL_MOUSE
 AC P97426;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Eosinophil cationic protein 1 precursor (EC 3.1.27.-) (ECP 1)
 DE (Ribonuclease 3-1) (Ribase 3-1) (Eosinophil secondary granule
 DE ribonuclease-1) (BAR-1).
 GN EARL.
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97057249; PubMed=8901588;
 RA Larson K.A., Olson E.V., Madden B.J., Gleich G.J., Lee N.A., Lee J.J.;
 RT Two highly homologous ribonuclease genes expressed in mouse
 RT superfamily. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12370-12375(1996).
 CC -1- FUNCTION: CYTOKIN AND HELMINTOTOXIN WITH RIBONUCLEASE ACTIVITY.
 CC POSSESSES A WIDE VARIETY OF BIOLOGICAL ACTIVITIES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MATRIX OF EOSINOPHIL'S LARGE SPECIFIC
 CC GRANULE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC

DR InterPro; IPR000822; Znf_C2H2.

DR SMART; SM00355; Znf_C2H2; 1.

DR EMBL; AC005785; AAC02838.1; -.

DR Genew; HGNC; 378; AKAP8.

DR MIM; 604692; -.

DR InterPro; IPR000822; Znf_C2H2.

DR SMART; SM00355; Znf_C2H2; 1.

KW Nuclear protein; Zinc-finger; DNA-binding.

FT DOMAIN 107 118 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 368 377 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT ZN_FING 392 414 C2H2-TYPE.

FT ZN_FING 481 504 C2H2-TYPE.

FT DOMAIN 572 589 RII-BINDING (BY SIMILARITY).

SQ SEQUENCE 692 AA; 76108 MW; CB0D5F014FD9B66 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 692; Best Local Similarity 80.0%; Pred. No. 1.9e-02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSQCR 5
|:|:
Db 170 YSECR 174

RESULT 9

ID	POLN_HEVME	STANDARD:	PRT;	1691 AA.
AC	POLN_HEVME			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Non-structural polyprotein [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Helicase].			
DE	Hepatitis E virus (strain Mexico) (HEV).			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Hepatitis E-like viruses.			
OC	OX NCBI_TaxID=31768;			
RN	[1]			
RF	SEQUENCE FROM N.A.			
RX	MEDLINE=93079857; PubMed=1448913; Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E., Bradley D.W., Tam A.W., Reyes G.R.; Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HEV)".			
RN	Virology 191:550-558(1992).			
RN	[2]			
RP	SEQUENCE OF 965-1691 FROM N.A.			
RX	MEDLINE=92211462; PubMed=1589964; Fry K.E., Tam A.W., Smith M.M., Kim J.P., Luk K.C., Young L.M., Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A., Bradley D.W., Reyes G.R.; Hepatitis E virus: strain variation in the nonstructural gene region encoding consensus motifs for an RNA-dependent RNA polymerase and an ATP/GTP binding site.";			
RN	Virus Genes 6:173-183(1992).			
CC	-1 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).			
CC	-1 MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF HEPATITIS E (ET-NANBH).			
CC	ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).			
CC	-----			
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CC	-----			
CC	EMBL; M73218; AAA45734.1; -.			
CC	PIR; A40778; MNWHE.			
CC	DR MEROPS; C41.001; -.			
CC	DR InterPro; IPR002589; Alpp.			
CC	DR InterPro; IPR0123; Phenylsite.			
CC	DR InterPro; IPR001788; RNA_dep_RNApol2.			
CC	DR InterPro; IPR002588; V_methyltransf.			
CC	DR InterPro; IPR000606; viral_helicase.			
CC	DR Pfam; PF00978; RNA Dep_RNApol2; 1.			
CC	DR Pfam; PF01443; viral_helicase; 1.			
CC	DR Pfam; PF01660; Vmethyltransf; 1.			
CC	DR SMART; SM00506; Alpp; 1.			
CC	DR Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.			
DR	NP_BIND 975 982 ATP (POTENTIAL).			

DR InterPro; IPR002589; Alpp.

DR InterPro; IPR001788; RNA_dep_RNApol2.

DR InterPro; IPR002588; V_methyltransf.

DR InterPro; IPR000606; viral_helicase.

DR Pfam; PF00978; RNA_dep_RNApol2; 1.

DR Pfam; PF01443; viral_helicase; 1.

DR Pfam; PF01660; Vmethyltransf; 1.

DR SMART; SM00506; Alpp; 1.

KW Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.

SEQUENCE	1693 AA;	185191 MW;	2F35546E9BDD219B CRC64;	ID	POLN_HEVVA	STANDARD;	PRT;	1693 AA.
Qy	1 YSOCR 5	:		AC	P3424;			
Db	431 YAQCR 435			DT	01-FEB-1994 (Rel. 28, Created)			
				DT	15-DEC-1998 (Rel. 37, Last sequence update)			
				DT	15-JUN-2002 (Rel. 41, Last annotation update)			
				DE	Non-structural polyprotein [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Helicase].			
				DE	Hepatitis E virus (strain Pakistan) (HEV).			
				OS	Viruses; ssRNA positive-strand viruses, no DNA stage;			
				OC	Hepatitis E-like viruses.			
				OX	NBII_TAXID=33774;			
				RN	[1]			
				RP	SEQUENCE FROM N.A.			
				RX	MDLINE=92115700; Published=1731327;			
				RA	Tsarev S.A., Emerson S.U., Revesz G.R., Tsareva T.S., Legters L.J.,			
				RA	Malik I.A., Iqbal M., Purcell R.H.;			
				RT	"Characterization of a prototype strain of hepatitis E virus.";			
				RL	Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).			
				CC	- - CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +			
				CC	(RNA) (N).			
				CC	- - MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF			
				CC	ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANB).			
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
				CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
				CC	the European Bioinformatics Institute. There are no restrictions on its			
				CC	use by non-profit institutions as long as its content is in no way			
				CC	modified and this statement is not removed. Usage by and for commercial			
				CC	entities requires license agreement. (See http://www.isb-sib.ch/announce/)			
				CC	or send an email to licensee@isb-sib.ch).			
				DR	EMBL: M80510; AAA45725.1; - .			
				DR	MEROPS: C41.001; - .			
				DR	InterPro: IPR002589; A1PP.			
				DR	InterPro: IPR001230; Preyl_site.			
				DR	InterPro: IPR0177; RNA_dep_RNAPol2.			
				DR	InterPro: IPR002588; V_methyltransf.			
				DR	InterPro: IPR000606; Viral_helicase1.			
				DR	PFAM: PF00978; RNA_dep_RNAPol2; 1.			
				DR	Pfam: PF01443; Viral_helicase1; 1.			
				DR	Pfam: PF01660; Vmethyltransf; 1.			
				DR	Pfam: PF01661; A1PP; 1.			
				DR	SMART: SM00506; A1PP; 1.			
				KW	Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase;			
				KW	ATP-binding.			
				FT	NP_BIND			
				FT	SEQUENCE 1693 AA;			
				FT	185149 MW;			
				FT	SA0F03FB1FB9E8 CRC64;			
				SO	Query Match	90.0%; Score 27; DB 1; Length 1693;		
				SO	Best Local Similarity 80.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;			
				Qy	1 YSOCR 5	:		
				Db	431 YAQCR 435			
					RESULT 13			
					RML6_MAIZE			
					ID RML6_MAIZE	STANDARD;	PRT;	185 AA.
					AC P27277;			
					DT 01-AUG-1992 (Rel. 23, Created)			
					DT 01-AUG-1992 (Rel. 23, Last sequence update)			
					DT 01-JUN-1994 (Rel. 29, Last annotation update)			
					DE Mitochondrial 60S ribosomal protein L16.			
					GN RPJ16.			
					OS Zea mays (Maize).			
					OG Mitochondrion.			
					OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
					OC Eukaryota; Monophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
					OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
					OC Palcoideae; Andropogoneae; Zea.			
					OX NCBI_TAXID=4577;			
					[1]			

RP SEQUENCE FROM N.A.
 RX MEDLINE=91216097; PubMed=1708720;
 RA Hunt M.D.; Newton K.J.;
 RT "The NCS3 mutation: genetic evidence for the expression of ribosomal protein genes in Zea mays mitochondria.";
 RL EMBL J. 10:1045-1052(1991).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: X57445; CAA0691_1; -.
 DR PIR: S15026; R52M6M.
 DR MaizDB: 69578; -.
 DR InterPro: IPR000114; Ribosomal_L16.
 DR Pfam: PF00252; RIBOSOMAL_L16; 1.
 DR PRINTS: PR00060; RIBOSOMAL_L16.
 DR TIGRFAMS: TIGR0116; rlp_bact; 1.
 DR PROSITE: PS00586; RIBOSOMAL_L16_1; 1.
 DR PROSITE: PS00701; RIBOSOMAL_L16_2; 1.
 DR KW Ribosomal Protein; Mitochondrial.
 SQ SEQUENCE 185 AA; F9CD590F773506A5 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 185;
 Best Local Similarity 80.0%; Pred. No. 1e+02; 1; Mismatches 4; Conservative 4; Indels 0; Gaps 0; Matches 1; Gaps 0; OX 1 YSKCR 5
 QY 1 YSKCR 57

Db 53 YSKCR 57

RESULT 14
 RM16_ORYSA STANDARD; PRT: 185 AA.
 AC P46B01;
 DT 01-NOV-1995 (Rel: 32, Created)
 DT 01-NOV-1995 (Rel: 32, Last sequence update)
 DT 01-NOV-1995 (Rel: 32, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L16.
 GN RPL16.
 OS Oryza sativa (Rice).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=CV_Nipponbare / Japonica; TISSUE=Leaf;
 RC MEDLINE=9530841; PubMed=7788722;
 RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyama M.,
 RA Hirai A.;
 RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is transcribed from alternative promoters.";
 RL Curr. Genet. 27:184-189(1995).
 RN [2] SEQUENCE OF 42-185 FROM N.A.
 RC STRAIN=CV_Nipponbare / Japonica;
 RX MEDLINE=95211362; PubMed=7545979;
 RA Itadani H., Wakasugi T., Sugiyama M., Nakazono M.,
 RA Hirai A.;
 RT "Nucleotide sequence of a 28 kbp portion of rice mitochondrial DNA: the existence of many sequences that correspond to parts of mitochondrial genes in intergenic regions.";
 RL Plant Cell Physiol. 35:1239-1244(1994).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.

CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: D21251; BA04793_1; -.
 DR PIR: D32052; BA05833_1; ALT TERM.
 DR InterPro: IPR000114; Ribosomal_L16.
 DR Pfam: PF00222; RIBOSOMAL_L16; 1.
 DR PRINTS: PR00060; RIBOSOMAL_L16.
 DR TIGRFAMS: TIGR01164; RLP_bact; 1.
 DR PROSITE: PS00586; RIBOSOMAL_L16_1; 1.
 DR PROSITE: PS00701; RIBOSOMAL_L16_2; 1.
 DR KW Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 185 AA; 20961 MW; 5FA75CDEF4C88539 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 185;
 Best Local Similarity 80.0%; Pred. No. 1e+02; 1; Mismatches 4; Conservative 4; Indels 0; Gaps 0; Matches 1; Gaps 0; OX 1 YSKCR 5
 QY 1 YSKCR 57

Db 53 YSKCR 57

RESULT 15
 Y460_PYRIO STANDARD; PRT: 188 AA.
 ID Y460_PYRHO
 AC 052115;
 DT 30-MAY-2000 (Rel: 39, Created)
 DT 30-MAY-2000 (Rel: 39, Last sequence update)
 DT 16-OCT-2001 (Rel: 40, Last annotation update)
 DE Hypothetical protein PH0460.
 GN PH0460.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 RN [1] Pyrococcus horikoshii.
 RP SEQUENCE FROM N.A.
 RC STRAIN=CP3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugii H., Haikawa Y., Hino Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuki Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kusihara N., Ooguchi A.,
 RA Aoki K.-I., Yoshikawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuechi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
 RT DNA Res. 5:55-76(1998).
 RL EMBL: APP0002; BAM29546_1; -.
 DR InterPro; IPR00462; CDP-OH_P_transf.
 DR Pfam: PF01066; CDP-OH_P_transf; 1.
 DR PROSITE; PS00179; CDP_ALCOHOL_P_TRANSF; 1.
 DR KW Hypothetical Protein; Transferase; Complete proteome.
 SQ SEQUENCE 188 AA; 20418 MW; D7EE6234216D3214 CRC64;

Thu Jul 10 13:20:53 2003

us-09-851-058-2.rsp

Page 8

Query Match 86.7%; Score 26; DB 1; Length 188;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
QY 1 YSQCR 5
||:||
Db 123 YSRCR 127

Search completed: July 9, 2003, 12:00:44
Job time : 8.75 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:57:21 ; Search time 17.75 Seconds

(without alignments)
58.041 Million cell updates/sec

Title: US-09-851-058-2
Perfect score: 30
Sequence: 1 YSQCR 5

Scanned:

671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRIMBLE_21; *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rabbit: *
12: sp_virus: *
13: sp_vertebrae: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SPTRIMBLE_21; *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

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14: sp_unclassified: *

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15: sp_rvirus: *

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7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

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15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

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10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

1: sp_archea: *

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5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

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11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

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17: sp_archaea: *

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4: sp_human: *

5: sp_invertebrate: *

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7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

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13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

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5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

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9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle: *

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10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp_rabbit: *

12: sp_virus: *

13: sp_vertebrae: *

14: sp_unclassified: *

15: sp_rvirus: *

16: sp_bacteriap: *

17: sp_archaea: *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_mhc: *

8: sp_organelle

DT 01-JUN-2002 (*TREMBlrel.* 21, Last annotation update)
DE Eosinophil-associated ribonuclease 2.
GN EAR2.
OS Mus paleari (Shrew mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TAXID=10093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RL Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RI Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238402; AAF67702.1; -.
DR HSSP; P00656; LSQ.
DR InterPro; IPR01427; RNASEA.
DR Pfam; PF0074; rnaseA; 1.
DR PRINTS; PRO0794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN 1.
SQ 154 AA; 17927 MW; 08F002D5B461DDF CRC64;

Query Match 100 %; Score 30; DB 11; Length 154;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOQR 5
Db 114 YSOQR 118

RESULT 3

Q9JKH6 PRELIMINARY; PRT; 155 AA.
ID Q9JKH6
AC 09JKH6;
DT 01-OCT-2000 (*TREMBlrel.* 15, Created)
DT 01-OCT-2000 (*TREMBlrel.* 15, Last sequence update)
DE Eosinophil-associated ribonuclease 2.
OS Mus caroli (Wild mouse) (Ricefield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RL Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RI Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238416; AAF67715.1; -.
DR HSSP; P00656; LSQ.
DR InterPro; IPR01427; RNASE.
DR Pfam; PF0074; rnaseA; 1.
DR PRINTS; PRO0794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN 1.
SQ 155 AA; 17420 MW; 56B351AA2B7B4551 CRC64;

Query Match 100 %; Score 30; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOQR 5
Db 115 YSOQR 119

RESULT 5

Q9JKG2 PRELIMINARY; PRT; 155 AA.
ID Q9JKG2
AC 09JKG2;
DT 01-OCT-2000 (*TREMBlrel.* 15, Created)
DT 01-OCT-2000 (*TREMBlrel.* 15, Last sequence update)
DE Eosinophil-associated ribonuclease 33.
OS Mus caroli (Wild mouse) (Ricefield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RL Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RI Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238422; AAF67721.1; -.
DR HSSP; P00656; LSQ.
DR InterPro; IPR01427; RNASE.
DR Pfam; PF0074; rnaseA; 1.
DR PRINTS; PRO0794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN 1.
SQ 155 AA; 17357 MW; C525FABBS19742 CRC64;

Query Match 100 %; Score 30; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOQR 5
Db 115 YSOQR 119

RESULT 4

Db	115		YSQCR 119
RESULT 6			
ID 062157	PRELIMINARY;	PRT;	221 AA.
AC 062157;			
DT 01-AUG-1998 (TREMBlrel. 07, Created)			
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE F1D1L_8 protein.			
GN F1D1L_8.			
OS Caenorhabditis elegans.			
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC Rhabditidae; Peloderrinae; Cenorhabditis;			
OX NCBI_TaxID=6239;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Mortimore B.J., Basham V.M.;			
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-99069613; Pubmed-98321916;			
RA none;			
RT "Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology.",			
RL Science 282:2012-2018(1998).			
DR EMBL; 281500; CAB40991; -;			
SQ SEQUENCE 221 AA; 2546 MW; 221F6EDF6844912F CRC64;			
Query Match 100.0%; Score 30; DB 5; Length 221;			
Best Local Similarity 100.0%; Pred. No. 21;			
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 YSQCR 5			
Db 107 YSQCR 111			
RESULT 7			
ID 09F03	PRELIMINARY;	PRT;	295 AA.
AC 09F03;			
DT 01-MAR-2001 ("TREMBrel. 16, Created)			
DT 01-MAR-2001 ("TREMBrel. 16, Last sequence update")			
DT 01-MAR-2002 ("TREMBrel. 20, Last annotation update")			
DE Putative branched-chain amino acid aminotransferase protein.			
GN OSJNBA0086P08 13.			
OS Oryza sativa (Rice).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzeae; Oryza.			
OX NCBI_TaxID=4530;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CV_NIPPONBARE;			
RA Sasaki T., Matsunoto T., Yamamoto K.;			
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:OSJNBA0086P08";			
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AP002855; BAB17203; -;			
DR InterPro; IPR01544; Aminotran_4.			
DR Pfam; PF01063; aminotran_4; 1.			
DR ProDom; PD001961; Aminotran_4; 1.			
KW Aminotransferase; Transferase;			
SQ SEQUENCE 295 AA; 31705 MW; 4C26272EB94100D9 CRC64;			
Query Match 100.0%; Score 30; DB 10; Length 295;			
Best Local Similarity 100.0%; Pred. No. 27;			
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 YSQCR 5			
Db 34 YSQCR 38			
RESULT 9			
ID 09AG1	PRELIMINARY;	PRT;	367 AA.
AC 09AG1;			
DT 01-JUN-2001 ("TREMBrel. 17, Created)			
DT 01-JUN-2002 ("TREMBrel. 21, Last annotation update")			
DE Hypothetical protein Xf0556.			
GN Xf0556.			
OS Xylella fastidiosa.			
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;			
OC Xylella.			
OX NCBI_TaxID=2371;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=AS5C;			
RX MEDLINE-2036517; PubMed-10910347;			
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aceacio M., Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barros M.H., Bacacorci E.D., Bordim S., Bove J.M., Brilhues M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Froime M., Furian L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kurama E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Macchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.Y., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D-H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Parisi A., Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E., de Sa R.G., Santelli R.V., Savasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A., de Souza A.P., Terenzio M.F., Truffi D., Tsai S.M., Tsuchako M.H., Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meladanis J., Setubal J.C., RT "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ," Nature 406:151-159(2000). DR EMBL; AE000390; AAC83366; 1. DR InterPro; IPR004881; DUF258. DR Pfam; PF03193; DUF258; 1. KW Hypothetical protein; Complete proteome. SQ SEQUENCE 341 AA; 37432 MW; 32AC71EPC7DDDF3A CRC64;			
Query Match 100.0%; Score 30; DB 16; Length 341;			
Best Local Similarity 100.0%; Pred. No. 31;			
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 YSQCR 5			
Db 34 YSQCR 38			

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomons.
 OC
 RN NCBI_TAXID=287;
 [1] SEQUENCE FROM N.A.
 RP
 RX MEDLINE=2137446; PubMed=11481492;
 RA Arora S.K., Bangera M., Lory S., Rampal R.;
 RT "A genomic island in *Pseudomonas aeruginosa* carries the determinants
 of flagellin glycosylation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9342-9347(2001).
 DR EMBL: AF32547; AK15337.1;
 DR InterPro; IPR000051; SAMBind.
 KW Hypothetical protein.
 SQ SEQUENCE 367 AA; 40811 MW; D83BE4716FCB2A7B CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 367;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 111 YSQCR 115

RESULT 10

094E22 PRELIMINARY; PRT; 555 AA.
 ID 094E22
 AC
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE Putative nucleoside triphosphatase.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eu dicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lam B., Soutchik A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kanaya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EML: AB3387012; AAC62457.1;
 DR InterPro; IPR00007; GDAI_CD39_WPase.
 DR Pfam; PF01120; GDAI_CD39_1;
 SQ SEQUENCE 555 AA; 631318 MW; D01A9FBD4C436962 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 555;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 349 YSQCR 353

RESULT 12

098440 PRELIMINARY; PRT; 78 AA.
 ID 098440
 AC
 DT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE A388R protein.
 GN A388R.
 OS *Paramecium bursaria chlorella virus 1* (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
 NCBI_TAXID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9600190; PubMed=8806566;
 RA Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.,
 RT "Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map
 positions 182 to 258.";
 RL Virology 223:303-317(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20013326; PubMed=10544099;
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Lisee A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homespermidine
 RT synthase.";
 RL Virology 263:254-262(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20478054; PubMed=11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
 PBCV-1.";
 RL Virology 275:27-35(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.

RA van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDJB databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V.; Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDJB databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V.; Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R.; Graves M.V.; Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDJB databases.
 DR EMBL: U42586; AAC96756; 1; -
 SQ SEQUENCE 78 AA; 9346 MW; 234659C398183E7F CRC64;
 Query Match 90.0%; Score 27; DB 12; Length 78;
 Best Local Similarity 80.0%; Pred. No. 40;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 27 YTQCR 31

RESULT 13

ID O9R130 PRELIMINARY; PRT; 153 AA.
 AC O9R130:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Ribonuclease 7 precursor (Fragment).
 GN R7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Domachowske J.B., Rosenberg H.F.;
 RT "Rapid evolution of the ribonuclease A superfamily: adaptive expansion
 of independent gene clusters in rats and mice.";
 RL Mol. Evol. 49:721-728(1999).
 DR EMBL: AF11645; AAD51661; 1; -
 HSSP: P00556; 2RNS.
 DR Interpro: IPR001427; RNaseA..
 DR Pfam: PF00074; rnasek_1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL 1
 FT CHAIN 26 >153 POTENTIAL.
 FT NON_TER 153 153 RIBONUCLEASE 7.
 SQ SEQUENCE 153 AA; 17679 MW; B5878251BA734D6B CRC64;

Query Match 90.0%; Score 27; DB 11; Length 153;
 Best Local Similarity 80.0%; Pred. No. 74;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQCR 5
 Db 113 YTQCR 117

RESULT 14

ID O9JK17 PRELIMINARY; PRT; 153 AA.

AC Q9JK17;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Bos taurus-associated ribonuclease 4.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mus saxicola (Spiny mouse).
 RL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang J.; Dyer K.D.; Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene
 family by rapid gene sorting and positive selection.";
 RT family by rapid gene sorting and positive selection.
 DR PROCB: NATL Acad. Sci. U.S.A. 97:4701-4706(2000).
 DR EMBL: AF238395; AAB67698; 1; -
 DR HSSP: P00656; 2RNS.
 DR InterPro: IPR001427; RNaseA..
 DR Pfam: PF00074; rnaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 SQ SEQUENCE 153 AA; 17042 MW; CFF9982F0A6AF296 CRC64;

Query Match 90.0%; Score 27; DB 11; Length 153;
 Best Local Similarity 80.0%; Pred. No. 74;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YSQCR 5
 Db 115 YTQCR 119

RESULT 15

ID O9R134 PRELIMINARY; PRT; 155 AA.
 AC O9R134;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Ribonuclease 1 precursor (Fragment).
 GN R1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20063779; PubMed=10594173;
 RA Singhmania N.A.; Dyer K.D.; Zhang J.; Deming M.S.; Bonville C.A.;
 RA Domachowske J.B.; Rosenberg H.F.;
 RT "Rapid evolution of the ribonuclease A superfamily: adaptive expansion
 of independent gene clusters in rats and mice.";
 RL Mol. Evol. 49:721-728(1999).
 DR EMBL: AF11641; AAD51661; 1; -
 DR HSSP: P00556; 2RNS.
 DR Interpro: IPR001427; RNaseA..
 DR Pfam: PF00074; rnase_1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW SIGNAL 1
 FT CHAIN 26 >153 RIBONUCLEASE 1.
 FT NON_TER 155 155
 SQ SEQUENCE 155 AA; 18119 MW; 16BA465D3260CEB CRC64;

Query Match 90.0%; Score 27; DB 11; Length 155;
 Best Local Similarity 80.0%; Pred. No. 75;

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us-09-851-058-2.rspt

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	Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy		1	YSOCR 5							
		:	III							
Db		115	YTOCR 119							

Search completed: July 9, 2003, 12:02:03
Job time: 19.75 secs

GenCore version 5.1.6
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On protein - protein search, using SW model

Run on: July 9, 2003, 11:55:35 ; Search time 22 Seconds
(without alignments)

30.284 Million cell updates/sec

Title: IUS-09-851-058-3
Perfect score: 31
Sequence: 1 YTOCR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	100.0	39 21	AAG12153 Arabidopsis thaliana
2	31	100.0	134 19	AAW59178 Rat eosinophil cat
3	31	100.0	155 19	AAW59177 Rat eosinophil cat
4	31	100.0	155 20	AAW94272 Rat-derived eosino
5	31	100.0	155 20	AAW94273 Rat eosinophils-de
6	28	90.3	44 23	ABP42832 Human ovarian anti
7	28	90.3	105 22	AAO10288 Human polypeptide
8	28	90.3	322 22	Propionibacterium
9	28	90.3	322 22	Propionibacterium
10	28	90.3	435 21	Arabidopsis
11	28	90.3	441 22	Drosophila melanog
12	28	90.3	476 22	Novel mar regulate
13	28	90.3	493 22	Novel human diagno
14	28	90.3	652 22	Drosophila melanog
15	28	90.3	856 22	C glutamic prote
16	27	87.1	35 20	Peptide sequence o
17	27	87.1	69 20	Clone 3 of A. thal
18	27	87.1	87 22	Human polypeptide
19	27	87.1	89 21	Arabidopsis thalia
20	27	87.1	159 22	Escherichia coli p
21	27	87.1	243 21	Rice branched chai
22	27	87.1	277 22	Human colon cancer
23	27	87.1	307 22	Human novel secret
24	27	87.1	337 21	Human prostate can
25	27	87.1	357 22	Drosophila melanog
26	27	87.1	442 21	Macaca mulatta rha
27	27	87.1	451 18	Human integrin-lin
28	27	87.1	452 22	Amino acid sequenc
29	27	87.1	452 23	Human integrin-lin
30	27	87.1	452 23	Human integrin-lin
31	27	87.1	452 23	Human integrin-lin
32	27	87.1	499 22	Novel human diagno
33	27	87.1	512 22	Novel human diagno
34	27	87.1	512 22	Novel human diagno
35	27	87.1	692 22	Human polypeptide,
36	27	87.1	692 22	Human integrin-lin
37	27	87.1	729 22	Human colon cancer
38	27	87.1	1122 20	Murine integrin-lin
39	27	87.1	1122 23	Mouse telomerase P
40	27	87.1	2174 22	Novel human diagno
41	27	87.1	2204 22	Novel human diagno
42	27	87.1	2204 22	Human polypeptide
43	26	83.9	42 21	TRAP20 homo
44	26	83.9	83 19	Arabidopsis thalia
45	26	83.9	48 19	Human semaphorin I
			50 22	Propionibacterium

ALIGNMENTS

D E Arabidopsis thaliana protein fragment SEQ ID NO: 11153.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression; control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.
XX EP1033405-A2.
PN EP1033405-A2.

PD 06-SEP-2000.
XX

PF 25-FEB-2000; 20000E0-0301439.

PR XX

PR 25-FEB-1999; 990US-0121825.

PR 05-MAR-1999; 990US-0121820.

PR 09-MAR-1999; 990US-012548.

PR 23-MAR-1999; 990US-012788.

PR 25-MAR-1999; 990US-0128264.

PR 29-MAR-1999; 990US-012785.

PR 01-MAR-1999; 990US-012462.

PR 06-MAR-1999; 990US-0128234.

PR 08-MAR-1999; 990US-012714.

PR 16-MAR-1999; 990US-0128845.

PR 19-APR-1999; 990US-0130077.

PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	21-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144884.
PR	28-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-0144814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR	04-MAY-1999;	99US-0132484.	PR	21-JUL-1999;	99US-0145088.
PR	05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145085.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145089.
PR	07-MAY-1999;	99US-0132853.	PR	22-JUL-1999;	99US-0145192.
PR	11-MAY-1999;	99US-0134226.	PR	23-JUL-1999;	99US-0145145.
PR	14-MAY-1999;	99US-0134219.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134221.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134370.	PR	26-JUL-1999;	99US-0145276.
PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145913.
PR	19-MAY-1999;	99US-0134941.	PR	27-JUL-1999;	99US-0145918.
PR	20-MAY-1999;	99US-0135124.	PR	28-JUL-1999;	99US-0145919.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146386.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146388.
PR	25-MAY-1999;	99US-0136021.	PR	02-AUG-1999;	99US-0146389.
PR	27-MAY-1999;	99US-0136592.	PR	03-AUG-1999;	99US-0147038.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147204.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147302.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147351.
PR	04-JUN-1999;	99US-0137502.	PR	05-AUG-1999;	99US-0147360.
PR	07-JUN-1999;	99US-0137724.	PR	05-AUG-1999;	99US-0147303.
PR	08-JUN-1999;	99US-0138094.	PR	06-AUG-1999;	99US-0147416.
PR	10-JUN-1999;	99US-0138540.	PR	03-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138847.	PR	09-AUG-1999;	99US-01474935.
PR	14-JUN-1999;	99US-0139119.	PR	10-AUG-1999;	99US-0147302.
PR	16-JUN-1999;	99US-0139452.	PR	11-AUG-1999;	99US-0147311.
PR	18-JUN-1999;	99US-0139453.	PR	12-AUG-1999;	99US-0148341.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148555.
PR	18-JUN-1999;	99US-0139454.	PR	13-AUG-1999;	99US-0148664.
PR	18-JUN-1999;	99US-0139455.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139456.	PR	17-AUG-1999;	99US-0149171.
PR	18-JUN-1999;	99US-0139457.	PR	18-AUG-1999;	99US-014926.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-014922.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139460.	PR	20-AUG-1999;	99US-014929.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139462.	PR	23-AUG-1999;	99US-0149330.
PR	18-JUN-1999;	99US-0139463.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139750.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139751.	PR	27-AUG-1999;	99US-015065.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-015066.
PR	22-JUN-1999;	99US-0139899.	PR	27-AUG-1999;	99US-015080.
PR	23-JUN-1999;	99US-0140353.	PR	30-AUG-1999;	99US-0151303.
PR	24-JUN-1999;	99US-0140354.	PR	31-AUG-1999;	99US-0151438.
PR	28-JUN-1999;	99US-0140695.	PR	01-SEP-1999;	99US-0151930.
PR	29-JUN-1999;	99US-0140823.	PR	07-SEP-1999;	99US-0153363.
PR	30-JUN-1999;	99US-0140991.	PR	10-SEP-1999;	99US-0153070.
PR	01-JUL-1999;	99US-0141287.	PR	13-SEP-1999;	99US-0153078.
PR	12-JUL-1999;	99US-0142977.	PR	15-SEP-1999;	99US-0154018.
PR	13-JUL-1999;	99US-0143512.	PR	16-SEP-1999;	99US-0154039.
PR	14-JUL-1999;	99US-0143624.	PR	20-SEP-1999;	99US-0154779.
PR	15-JUL-1999;	99US-0144055.	PR	22-SEP-1999;	99US-0155139.
PR	16-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	16-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0144066.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0144335.	PR	29-SEP-1999;	99US-0156596.
PR	19-JUL-1999;	99US-0144332.	PR	04-OCT-1999;	99US-0157117.
PR	19-JUL-1999;	99US-0144333.	PR	05-OCT-1999;	99US-0157753.
PR	19-JUL-1999;	99US-0144334.	PR	06-OCT-1999;	99US-0157865.
PR	19-JUL-1999;	99US-0144335.	PR	07-OCT-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144335.	PR	12-OCT-1999;	99US-0158329.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.

PR 14-OCT-1999; 99US-015331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-015584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160985.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 31; DB 21; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTQCR 5
 Db 94 YTQCR 98

Db 14 YTQCR 18

RESULT 2

AAW59178 standard; Protein: 134 AA.
 ID AAW59178
 AC AAW59178;
 DT 13-AUG-1998 (first entry)

XX Rat eosinophil cationic protein #2.
 XX Eosinophil cationic protein; ECP; cytotoxic; recombinant protein;
 KW treatment; disease; rat.
 XX Rattus sp.
 XX PN JPL0117777-A.
 XX PD 12-MAY-1998.
 XX PF 25-OCT-1996; 96JP-0284311.
 XX PR 25-OCT-1996; 96JP-0284311.
 XX DR N-PSDB; AAV11934, AAV11935.
 XX PT New DNA coding rat-derived eosinophil cationic protein - used, e.g.
 PT to produce recombinant protein for treatment of diseases
 XX PS Claim 3; Page 9-10; 14pp; Japanese.
 XX CC This sequence is a novel rat-derived eosinophil cationic protein (ECP)
 CC which exhibits cytotoxic activity. The DNA encoding the ECP protein
 CC can be used for the production of recombinant protein which is useful
 CC for the treatment of diseases.
 XX SQ Sequence 155 AA:

Query Match 100.0%; Score 31; DB 19; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTQCR 5
 Db 115 YTQCR 119

RESULT 4

AAW94272 standard; Protein: 155 AA.
 ID AAW94272
 AC AAW94272;
 DT 22-APR-1999 (first entry)

XX Rat-derived eosinophil-derived neurotoxin (EDN).
 XX DE Rat-derived eosinophil-derived neurotoxin (EDN).
 XX EDN Eosinophil-derived neurotoxin; EDN; eosinophil cationic protein; ECP;
 KW recombinant; rat; precursor.
 XX OS Rattus sp.
 XX PN JPL1009280-A.

XX This sequence is a novel rat-derived eosinophil cationic protein (ECP)
 CC which exhibits cytotoxic activity. The DNA encoding the ECP protein
 CC can be used for the production of recombinant protein which is useful
 CC for the treatment of diseases.
 XX SQ sequence 134 AA;

Query Match 100.0%; Score 31; DB 19; Length 134;

XX
 PD 19-JAN-1999.
 XX
 PF 25-JUN-1997; 97JP-0169271.
 XX
 PR 25-JUN-1997; 97JP-0169271.
 XX
 PA (NIHA) JAPAN ENERGY CORP.
 XX
 DR WPI; 1999-145897/13.
 XX
 DR N-PSDB; AAX05636, AAX05637.
 XX
 PT New rat-derived eosinophil-derived neurotoxin gene - useful for
 PT preparing recombinant protein
 XX
 PS Claim 1; Page 10; 18pp; Japanese.
 XX
 CC This represents a rat-derived eosinophil-derived neurotoxin gene - useful for
 CC DNA coding rat-derived EDN or its precursor peptide is useful for the
 CC preparation of a recombinant protein. The base sequence of a precursor peptide of rat eosinophil-
 CC derived ECP, and the base sequence of the precursor peptide of EDN can
 CC be determined by collecting the ECP cDNA and EDN cDNA from eosinophils
 CC respectively.
 XX
 SQ Sequence 155 AA;
 Query Match 100.0%; Score 31; DB 20; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 |||||
 Db 115 YTQCR 119
 RESULT 5
 AAW94273
 ID AAW94273 standard; Protein; 155 AA.
 XX
 AC AAW94273;
 XX
 DT 22-APR-1999 (first entry)
 XX
 DE Rat eosinophil-derived eosinophil cationic protein (ECP).
 XX
 KW Eosinophil-derived neurotoxin; EDN; eosinophil cationic protein; ECP;
 KW recombinant; rat; precursor.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 59
 FT /note= "indicated as Cys in the sequence listing"
 FT Peptide 99
 FT /note= "indicated as Val in the sequence listing"
 XX
 PN .JP11009280-A.
 XX
 PD 19-JAN-1999.
 XX
 PR 25-JUN-1997; 97JP-0169271.
 XX
 PA (NIHA) JAPAN ENERGY CORP.
 XX
 DR WPI; 1999-145897/13.
 XX
 DR N-PSDB; AAX05638.
 XX
 PT New rat-derived eosinophil-derived neurotoxin gene - useful for
 PT preparing recombinant protein
 XX
 PS Disclosure; Fig 4; 18pp; Japanese.
 XX
 CC This represents a rat eosinophils-derived eosinophil cationic protein
 CC (ECP). The DNA encoding a rat-derived eosinophil-derived neurotoxin (EDN)
 CC or its precursor peptide is useful for the preparation of a recombinant
 CC protein. The base sequence of a precursor peptide of rat eosinophil-
 CC derived ECP, and the base sequence of the precursor peptide of EDN can
 CC be determined by collecting the ECP cDNA and EDN cDNA from eosinophils
 CC respectively.
 XX
 SQ Sequence 155 AA;
 Query Match 100.0%; Score 31; DB 20; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 |||||
 Db 115 YTQCR 119
 RESULT 6
 ABP42832
 ID ABP42832 standard; Protein; 44 AA.
 XX
 AC ABP42832;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HPCPH68, SEQ ID NO:3964.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; respiratory disorder; blood disorder;
 KW cardiovascular disorder; urinary system disorder; drug screening;
 KW gastrointestinal disorder; chromosome mapping; forensic analysis;
 KW gene therapy; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PR 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 XX
 DR N-PSDB; ABQ5599.
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.,
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 11; SEQ ID NO 3964; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP41322B), and to cDNAs encoding them (ABQ5131-ABQ5305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosis or preventing various ovarian and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoeal), endocrine
 CC disorders, infectious (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC poly nucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The poly nucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC poly peptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention.
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SEQ ID NO: 24180; SEQ ID NO: 24180; SEQ ID NO: 24180; SEQ ID NO: 24180;

Query Match 90.3%; Score 28; DB 23; Length 44;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTOCR 5
 |||||
 Db 25 YTECR 29

RESULT 7
 AA01288
 ID AA01288 standard; Protein: 105 AA.
 XX
 AC AA01288;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human Polypeptide SEQ ID NO: 24180.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX
 WO200164035-A2.

XX
 PR 0200164035-A2.

XX
 PD 07-SEP-2001.

XX
 PR 26-FEB-2001; 2001WO-US04927.

XX
 PR 28-FEB-2000; 2000US 0515126.

XX
 PR 18-MAY-2000; 2000US-0577409.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Tang YT, Liu C, Drmanac RT;

XX
 DR WPI: 2001-514838/56.

DR N-P5DB; AA190219.

XX
 PT isolated nucleic acids and poly peptides, useful for preventing

PT diagnosing and treating e.g. leukaemia, inflammation and immune

PT disorders.

XX
 PS Claim 20; SEQ ID NO 24180; 1399pp + Sequence Listing; English.

XX
 The invention relates to human poly nucleotides (AA179941-AA193841) and

the encoded proteins (AA000010-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The poly nucleotides and poly peptides are useful in gene therapy, vaccines or peptide therapy. The poly peptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SEQ ID NO: 24180; SEQ ID NO: 24180; SEQ ID NO: 24180; SEQ ID NO: 24180;

Query Match 90.3%; Score 28; DB 22; Length 105;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTOCR 5
 |||||
 Db 17 YTECR 21

RESULT 8
 AAU44616 standard; Protein: 322 AA.
 ID AAU44616
 XX
 AC AAU44616;
 XX
 DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #5512.
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopatological; neuroprotectant.

XX
 OS Propionibacterium acnes.

XX
 PN WO200181581-A2.

XX
 PD 01-NOV-2001.

XX
 PR 20-APR-2001; 2001WO-US12865.

XX
 PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US 208811P.

PR 07-JUL-2000; 2000US-216747P.

XX
 PA (CORI-) CORIXA CORP.

XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX
 DR WPI: 2001-616774/71.

DR N-P5DB; AA559523.

PT Propionibacterium acnes poly peptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX
 PS Example 1; SEQ ID NO 5811; 1069pp; English.

XX
 CC sequences AAU39105-AAU68017 represent propionibacterium acnes immunogenic

CC poly peptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteoarthritis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with *acne vulgaris*. A method for detecting the presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences.

CC sequence 322 AA;

CC

Query Match Similarity 90.3%; Score 28; DB 22; Length 322; Best Local Similarity 80.0%; Pred. No. 1.2e+03; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTOCR 5
Db 148 YTECR 152

RESULT 9
AAG24041
ID AAG24041 standard; Protein; 435 AA.

XX AC AAG24041;
XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 27556.

KW protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 990S-0118025.
PR 05-MAR-1999; 990S-0133180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127452.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 26-APR-1999; 990S-0130891.
PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 04-MAY-1999; 990S-0132484.
PR 05-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 07-MAY-1999; 990S-0132487.
PR 11-MAY-1999; 990S-0132483.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.

PR 14-MAY-1999; 990S-0134370.	PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0134941.	PR 20-MAY-1999; 990S-0155124.
PR 21-MAY-1999; 990S-0135353.	PR 24-MAY-1999; 990S-0155629.
PR 25-MAY-1999; 990S-0136021.	PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.	PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.	PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.	PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.	PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.	PR 18-JUN-1999; 990S-0139453.
PR 17-JUN-1999; 990S-0139454.	PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.	PR 18-JUN-1999; 990S-0139457.
PR 18-JUN-1999; 990S-0139458.	PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139817.	PR 18-JUN-1999; 990S-0139840.
PR 18-JUN-1999; 990S-0139899.	PR 18-JUN-1999; 990S-0139962.
PR 18-JUN-1999; 990S-0140353.	PR 18-JUN-1999; 990S-0140354.
PR 18-JUN-1999; 990S-0140695.	PR 18-JUN-1999; 990S-0140750.
PR 18-JUN-1999; 990S-0140823.	PR 18-JUN-1999; 990S-0140951.
PR 28-JUN-1999; 990S-0140991.	PR 29-JUN-1999; 990S-0141287.
PR 29-JUN-1999; 990S-0141287.	PR 30-JUN-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.	PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.	PR 08-JUL-1999; 990S-0142803.
PR 08-JUL-1999; 990S-0142803.	PR 09-JUL-1999; 990S-0142920.
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RESULT 10
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 KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
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PD 11-OCT-2001.
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 PF 30-MAR-2001; 2001WO-US08631.
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 PR 23-AUG-2000; 2000US-0549167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 XX
 N-PSDB; AAS09231.

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX
 PS Claim 20; SEQ ID NO 55403; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABC0010-ABC30377 represent novel human diagnostic amino acid sequences. The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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 PN WO200171042-A2.
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 PD 27-SEP-2001.
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 PP 18-DEC-2000; 2000EP-0127688.
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 PR 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159162.
 PR 03-AUG-2000; 2000JP-0280988.
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 PA (KYOWA) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
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 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
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 DR WPI; 2001-375931/40.
 DR N-PSDB; AAH64980.

XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing gene
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX

PS Claim 17; SEQ ID NO: 3515; 246pp + Sequence Listing; English.

XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the coryneform bacterium *Corynebacterium glutamicum*. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-Lysine. The present sequence is a protein described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX

SQ Sequence 856 AA;

Query Match 90.3%; Score 28; DB 22; Length 856;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Title: US-09-851-058-3

Perfect score: 31

Sequence: 1 YTQCR 5

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Post-processing: Minimum Match 0%

Maximum Match 100%

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7	26	83.9	562 6	US-08-258-502-2
8	26	83.9	651 1	US-08-264-101-2
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ALIGNMENTS

RESULT 1

US-09-173-300-22
; Sequence 22, Application US/09173300

GENERAL INFORMATION:

APPLICANT: Falco, Saverio Carl

APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.

APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES

FILE REFERENCE: BB-1126
CURRENT FILING DATE: 1998-10-15

EARLIER APPLICATION NUMBER: 60/063,423

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Microsoft Word Version 7.0A

SEQ ID NO 22
LENGTH: 243

TYPE: PRT
ORGANISM: Glycine max

US-09-173-300-22

Query Match

Best Local Similarity 80.0%; Pred. No. 2.6e-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTQCR 5
|:|||

Db 68 YTQCR 72

RESULT 2

US-09-035-706-2
; Sequence 2, Application US/09035706

GENERAL INFORMATION:

APPLICANT: Dedhar, Shoukat

APPLICANT: Hannigan, Greg

TITLE OF INVENTION: Integrin-Linked Kinase and

TITLE OF INVENTION: Its Uses

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Avenue, Suite 200

CITY: Palo Alto

STATE: CA

ZIP: USA

ZIP: 94301

US-09-566-906-2

Query Match Best Local Similarity Score DB Length
 87.1%; 80.0%; 27; 4; 452;

Matches Pred. No. Mismatches Indels Gaps 0;
 4; 0; 0; 0; 0;

Qy 1 YTQCR 5
 Db 5 FTQCR 9

RESULT 6
 US-09-238-796-2
 Sequence 2, Application US/09238796

GENERAL INFORMATION:
 APPLICANT: ALYAR, NAMBI V.
 TITLE OF INVENTION: BECRLR; BOVINE CALCITONIN RECEPTOR-LIKE
 TITLE OF INVENTION: RECEPTOR
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rattner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTKEY FOR WINDOWS Version 2.0
 APPLICATION NUMBER: US/09/238,796

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 28-JAN-1999

ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-70599
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 462 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

;
 US-09-238-796-2
 Query Match Best Local Similarity Score DB Length
 83.9%; 100.0%; 26; 3; 462;

Matches Pred. No. Mismatches Indels Gaps 0;
 4; 0; 0; 0; 0;

Qy 1 YTQCR 4
 Db 125 YTQCR 128

RESULT 7
 528502-2

PATENT NO. 528502
 APPLICANT: Kuranda, Michael J.
 TITLE OF INVENTION: IMMOBILIZATION AND PURIFICATION OF
 FUSION PROTEINS USING CHITIN-BINDING ABILITY
 NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/303,827

Query Match Best Local Similarity Score DB Length
 83.9%; 100.0%; 26; 6; 562;

Matches Pred. No. Mismatches Indels Gaps 0;
 4; 0; 0; 0;

Qy 1 YTQC 4
 Db 549 YTQC 552

RESULT 8
 US-08-264-101-2
 Sequence 2, Application US/08264101

GENERAL INFORMATION:
 APPLICANT: ALVES, KENNETH
 APPLICANT: GUPTA, SUNIL K.
 APPLICANT: HOLLISS, GREGORY F.
 TITLE OF INVENTION: CONTRACEPTIVE VACCINE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MARY A. APPOLLINA
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: Rahway
 STATE: NJ USA
 ZIP: 07065

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC/DO/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/264,101

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: APPOLLINA, MARY A.

REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19244
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-3462
 TELEX: (908)594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 651 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

;
 US-08-264-101-2
 Query Match Best Local Similarity Score DB Length
 83.9%; 100.0%; 26; 1; 651;

Matches Pred. No. Mismatches Indels Gaps 0;
 4; 0; 0; 0; 0;

Qy 1 YTQC 4
 Db 448 YTQC 451

US-09-851-058-3.rai

Query Match Best Local Similarity Score DB Length
 83.9%; 100.0%; 26; 6; 562;

Matches Pred. No. Mismatches Indels Gaps 0;
 4; 0; 0; 0;

Qy 1 YTQC 4
 Db 549 YTQC 552

RESULT 9
 US-08-765-243-2
 Sequence 2, Application US/08765243

GENERAL INFORMATION:
 APPLICANT: ALVES, KENNETH

APPLICANT: GUPTA, SUNIL K.
 APPLICANT: HOLLISS, GREGORY F.
 TITLE OF INVENTION: CONTRACEPTIVE VACCINE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MARY A. APPOLLINA
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAILWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/765,243
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: APPOLLINA, MARY A
 REFERENCE/DOCKET NUMBER: 34,087
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-3462
 TELEX/FAX: (908)594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 651 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

PCT-US95/07295-2
 RESULT 10
 Query Match 83.9%; Score 26; DB 2; Length 651;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQC 4
 Db 448 YTQC 451

RESULT 11
 US/08/765,243-8
 Sequence 8, Application US/08/765243
 PATENT NO. 593578
 GENERAL INFORMATION:
 APPLICANT: ALVES, KENNETH
 APPLICANT: GUPTA, SUNIL K.
 APPLICANT: HOLLISS, GREGORY F.
 TITLE OF INVENTION: CONTRACEPTIVE VACCINE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MARY A. APPOLLINA
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAILWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/765,243
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: APPOLLINA, MARY A
 REFERENCE/DOCKET NUMBER: 34,087
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-3462
 TELEX/FAX: (908)594-4720
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 734 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US/08/765,243-8
 RESULT 12
 Query Match 83.9%; Score 26; DB 2; Length 734;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQC 4
 Db 531 YTQC 534

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07295
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: APPOLLINA, MARY A
 REFERENCE/DOCKET NUMBER: 34,087

PCT-US95-07295-8

Sequence 8, Application PC/TUS9507295

GENERAL INFORMATION:

APPLICANT: ALVES, KENNETH

APPLICANT: GUPTA, SUNIL K.

TITLE OF INVENTION: CONTRACEPTIVE VACCINE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARK A. APPOLLINA

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07295

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: APPOLLINA, MARY A.

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 19244Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3462

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 734 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-07295-8

Db 917 YTOC 920 ||||

RESULT 14

US-09-463-702A-2

Sequence 2, Application US/09463702A

Patent No. 6335435

GENERAL INFORMATION:

APPLICANT: AGENE Research Institute, Co., Ltd.

APPLICANT: HIRAKI AND ASSOCIATES

APPLICANT: SHIMAMOTO, AKIRO

APPLICANT: KITAO, SAORI

APPLICANT: FURUCHI, YASUHIRO

TITLE OF INVENTION: HUMAN GENE RECO4 ENCODING HELICASE

FILE REFERENCE: HIRAI150

CURRENT APPLICATION NUMBER: US/09/463,702A

CURRENT FILING DATE: 2000-01-24

PRIOR APPLICATION NUMBER: PCT/JP98/03114

PRIOR FILING DATE: 1998-07-10

PRIOR APPLICATION NUMBER: JAPAN 9/200387

PRIOR FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 1208

TYPE: PRT

ORGANISM: Homo sapiens

US-09-463-702A-2

Query Match 83.9%; Score 26; DB 4; Length 1208;

Best Local Similarity 80.0%; Pred. No. 1.3e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YTOC 5

Db 942 YHCR 946

Db 917 YTOC 920 ||||

RESULT 15

US-09-191-647-2

Sequence 2, Application US/09191647

Patent No. 6046015

GENERAL INFORMATION:

APPLICANT: Goodman, Corey

APPLICANT: Kid, Thomas

APPLICANT: Brose, Katja

APPLICANT: Tessier-Lavigne, Marc

TITLE OF INVENTION: Modulating Robo: Ligand Interactions

FILE REFERENCE: B98-031-3

CURRENT APPLICATION NUMBER: US/09/191,647

CURRENT FILING DATE: 1998-11-13

EARLIER APPLICATION NUMBER: 60/065,544

EARLIER FILING DATE: 1997-11-14

EARLIER APPLICATION NUMBER: 60/081,057

EARLIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin ver. 2.0

SEQ ID NO 2

LENGTH: 1525

TYPE: PRT

ORGANISM: human

US-09-191-647-2

Query Match 83.9%; Score 26; DB 3; Length 1525;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YTOC 4

Db 233 YTOC 236

Query Match 83.9%; Score 26; DB 2; Length 1005;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YTOC 4

Organism: Homo sapiens

US-08-935-450-2

Query Match 83.9%; Score 26; DB 5; Length 734;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YTOC 4

Db 531 YTOC 534

RESULT 13

US-08-935-450-2

Sequence 2, Application US/08935450

GENERAL INFORMATION:

APPLICANT: Rambabai, Krishnan

APPLICANT: Yang, Meijia

APPLICANT: Schulz, Vincent

TITLE OF INVENTION: 53bp2 COMPLEXES

FILE REFERENCE: 7934-054

CURRENT APPLICATION NUMBER: US/08/935,450

CURRENT FILING DATE: 1997-03-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 1005

TYPE: PRT

ORGANISM: Homo sapiens

US-08-935-450-2

Query Match 83.9%; Score 26; DB 2; Length 1005;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YTOC 4

Db 233 YTOC 236

Thu Jul 10 13:20:58 2003

Search completed: July 9, 2003, 12:03:37
Job time : 12.25 secs

us-09-851-058-3.ra1

Page 1

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GenFore Version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:02:11 ; search time 20.25 Seconds
(without alignments)

28.746 Million cell updates/sec

Title: US-09-851-058-3

Perfect score: 31 YTCR 5

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 11619773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA,*

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2: /cgn2_6/ptodata/1/pubpba/US06_NEW_PUB_pep:*

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11: /cgn2_6/ptodata/1/pubpba/US10_NEW_PUB_pep:*

12: /cgn2_6/ptodata/1/pubpba/US10_PUBOMB_pep:*

13: /cgn2_6/ptodata/1/pubpba/US00_NEW_PUB_pep:*

14: /cgn2_6/ptodata/1/pubpba/US60_PUBOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	28	90.3	818	9 US-10-156-761-9960	Sequence 9960, AP
2	28	90.3	856	9 US-09-738-626-3515	Sequence 3515, AP
3	27	87.1	243	12 US-10-027-450-22	Sequence 22, APPL
4	27	87.1	277	9 US-10-106-698-5823	Sequence 5823, AP
5	27	87.1	307	10 US-09-764-864-1222	Sequence 1222, AP
6	27	87.1	337	10 US-09-25-300-1708	Sequence 1708, AP
7	27	87.1	452	10 US-09-840-704-2	Sequence 2, APPL
8	27	87.1	643	9 US-10-198-070-43	Sequence 43, APPL
9	27	87.1	700	9 US-09-906-419-17	Sequence 17, APPL
10	27	87.1	700	9 US-10-119-136-17	Sequence 17, APPL
11	27	87.1	700	9 US-10-119-136-130	Sequence 130, APPL
12	27	87.1	729	9 US-10-106-698-6364	Sequence 6364, APPL
13	26	83.9	529	9 US-10-106-698-7543	Sequence 7543, APPL
14	26	83.9	64	10 US-09-864-761-34561	Sequence 34561, APPL
15	26	83.9	68	9 US-10-083-357-1024	Sequence 1024, APPL
16	26	83.9	139	9 US-10-125-540-521	Sequence 521, APPL
17	26	83.9	139	10 US-09-764-870-521	Sequence 521, APPL
18	26	83.9	158	9 US-10-295-403-118	Sequence 118, APPL
19	26	83.9	9 US-10-156-761-8563	Sequence 8563, APPL	

ALIGNMENTS

RESULT 1

US-10-156-761-9960

; Sequence 9960, Application US/10156761

; Publication No. US200301190181

; GENERAL INFORMATION:

; APPLICANT: OOURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAI, YOSHIOKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156-761

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 9960

LENGTH: 818

TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-9960

Query Match 90.3%; Score 28; DB 9; Best Local Similarity 80.0%; Score 28; DB 9; Matches 4; Conservative 1; Mismatches 0

QY 1 YTCR 5 |:|||

Db 133 YTCR 137

RESULT 2

US-09-738-626-3515

; Sequence 3515, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

SUMMARIES

RESULT 4
US-10-106-698-5823
; Sequence 5823, Application US/10106698
; Publication No. US20030109690A1

Query Match, Best Local Similarity 80.0%; Pred. No. 4.3e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 68 YSOQR 72

TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3515

Query Match, Best Local Similarity 90.3%; Score 28; DB 9; Length 856;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 126 YTECR 130

RESULT 3
US-10-027-450-22
; Sequence 22, Application US/10027450
; Patent No. US20030102715A1

GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Falco, Saverio Carl
APPLICANT: Kinney, Anthony J.
APPLICANT: Canoan, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-126
CURRENT APPLICATION NUMBER: US710/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 22
LENGTH: 243
TYPE: PRT
; ORGANISM: Glycine max
US-10-027-450-22

Query Match, Best Local Similarity 80.0%; Pred. No. 4.3e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 68 YSOQR 72

RESULT 5
US-09-764-864-1222
; Sequence 122, Application US/09764864
; Patent No. US20030132753A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT723
CURRENT APPLICATION NUMBER: US/09764,864
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09764,864
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122
LENGTH: 307
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (283)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (293)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1222

Query Match, Best Local Similarity 80.0%; Pred. No. 5.4e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 16 YTQCO 20

RESULT 6
US-09-925-300-1708
; Sequence 1708, Application US/09925300
; Patent No. US20030151681A1
; GENERAL INFORMATION:

APPLICANT: Craig Rosen,
 APPLICANT: Steve Ruben
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIORITY APPLICATION NUMBER: PCT/US00/05988
 PRIORITY FILING DATE: 2000-03-08
 PRIORITY APPLICATION NUMBER: 60/124,270
 PRIORITY FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1890
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 1708
 LENGTH: 337
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (112)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (127)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (283)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-300-1708

Query Match 87.1%; Score 27; DB 10; Length 337;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHQCR 5
 Db 16 YHQCR 20

RESULT 7
 US-09-840-704-2
 ; Sequence 2, Application US/09840704
 ; Patent No. US20020122801A1
 ; GENERAL INFORMATION
 ; APPLICANT: Deodhar, Shonkat
 ; APPLICANT: Hannigan, Greg
 ; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
 ; FILE REFERENCE: KIN-2CON
 ; CURRENT APPLICATION NUMBER: US/09/840,704
 ; CURRENT FILING DATE: 2001-04-23
 ; PRIORITY APPLICATION NUMBER: 09/566,906
 ; PRIORITY FILING DATE: 2000-05-09
 ; PRIORITY APPLICATION NUMBER: US08/752,345
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 452
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-840-704-2

Query Match 87.1%; Score 27; DB 10; Length 452;
 Best Local Similarity 80.0%; Pred. No. 7.6e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 5 1111

RESULT 8
 US-10-198-070-43
 ; Sequence 43, Application US/10198070
 ; Publication No. US20030109437A1

RESULT 9
 US-09-906-419-17
 ; Sequence 17, Application US/09906419
 ; Publication No. US20030037373A1
 ; GENERAL INFORMATION
 ; APPLICANT: Shockey, Jay
 ; APPLICANT: Schnurr, Judy
 ; APPLICANT: Bwse, John
 ; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
 ; FILE REFERENCE: DOW-04679
 ; CURRENT APPLICATION NUMBER: US/09/906,419
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIORITY APPLICATION NUMBER: 60/220,474
 ; PRIORITY FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 700
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-906-419-17

Query Match 87.1%; Score 27; DB 9; Length 643;
 Best Local Similarity 80.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 523 YTQCR 527

RESULT 10
 US-10-119-136-17
 ; Sequence 17, Application US/1019136
 ; Publication No. US20030097676A1
 ; GENERAL INFORMATION
 ; APPLICANT: Shockey, Jay
 ; APPLICANT: Schnurr, Judy
 ; APPLICANT: Browne, John
 ; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
 ; FILE REFERENCE: DOW-04695

CURRENT APPLICATION NUMBER: US/10/119,136
 CURRENT FILING DATE: 2002-03-04
 PRIORITY APPLICATION NUMBER: 09/906,419
 PRIORITY FILING DATE: 2001-07-15
 PRIORITY APPLICATION NUMBER: 60/220,474
 NUMBER OF SEQ ID NOS: 132
 SEQ ID NO 17
 LENGTH: 700
 SOFTWARE: PatentIn version 3.0
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-119-136-17

Query Match 87.1%; Score 27; DB 9; Length 700;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 570 YTQCR 574

RESULT 11
 US-10-119-136-130
 Sequence 130, Application US/10/119135
 Publication No. US20030097676A1
 GENERAL INFORMATION:
 APPLICANT: Shockey, Jay
 APPLICANT: Schnurr, Judy
 APPLICANT: Browne, John
 TITLE OF INVENTION: Plant Acyl-CoA Synthetases
 FILE REFERENCE: DOW-04695
 CURRENT APPLICATION NUMBER: US/10/119,136
 CURRENT FILING DATE: 2002-09-04
 PRIORITY FILING DATE: 2001-07-16
 PRIORITY APPLICATION NUMBER: 09/906,419
 PRIORITY FILING DATE: 2000-07-21
 PRIORITY APPLICATION NUMBER: US/10/119,136
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 132
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 130
 LENGTH: 700
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-119-136-130

Query Match 87.1%; Score 27; DB 9; Length 700;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 570 YTQCR 574

RESULT 12
 US 10-106-698-6364
 Sequence 6364, Application US/10/06698
 Publication No. US20030109690A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
 FILE REFERENCE: PA005P1
 CURRENT APPLICATION NUMBER: US/10/106,698
 CURRENT FILING DATE: 2002-03-27
 PRIORITY FILING DATE: 2000-09-28
 PRIORITY APPLICATION NUMBER: US 60/157,137
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO 7543
 LENGTH: 52
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-698-7543

Query Match 87.1%; Score 27; DB 9; Length 700;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 570 YTQCR 574

RESULT 13
 US 10-106-698-7543
 Sequence 7543, Application US/10/06698
 Publication No. US20030109690A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
 FILE REFERENCE: PA005P1
 CURRENT APPLICATION NUMBER: US/10/106,698
 CURRENT FILING DATE: 2002-03-27
 PRIORITY FILING DATE: 2000-09-28
 PRIORITY APPLICATION NUMBER: US 60/157,137
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO 7543
 LENGTH: 52
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-698-7543

Query Match 87.1%; Score 27; DB 9; Length 700;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 29 YNQCR 33

RESULT 14
 US-09-864-761-34561
 Sequence 34561, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David R.
 APPLICANT: Chen, Weisheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aeonlica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 2000-09-28
 PRIORITY APPLICATION NUMBER: US 60/157,137
 PRIORITY FILING DATE: 1999-09-29
 PRIORITY APPLICATION NUMBER: US 60/163,280
 PRIORITY FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 PRIORITY APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26 ; NUMBER OF SEQ ID NOS: 1346
 PRIOR APPLICATION NUMBER: US 09/632,366 ; SEQ ID NO 1024
 PRIOR FILING DATE: 2000-08-03 ; LENGTH: 68
 PRIOR APPLICATION NUMBER: GB 24263,6 ; TYPE: PRT
 PRIOR FILING DATE: 2000-10-04 ;
 PRIOR APPLICATION NUMBER: US 60/236,359 ; ORGANISM: *Saccharomyces cerevisiae*
 PRIOR FILING DATE: 2000-09-27 ; US-10-033-357-1024
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30 ; Query Match 83.9%; Score 26; DB 9; Length 68;
 PRIOR APPLICATION NUMBER: PCT/US01/00667 ; Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 PRIOR FILING DATE: 2001-01-30 ; Matches 4; Conservative 0; Mismatches 0; Indels 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00664 ; Gaps 0;
 PRIOR FILING DATE: 2001-01-30 ; Gaps 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00668 ; Gaps 0;
 PRIOR FILING DATE: 2001-01-30 ; Gaps 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00663 ; Gaps 0;
 PRIOR FILING DATE: 2001-01-30 ; Gaps 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00662 ; Gaps 0;
 PRIOR FILING DATE: 2001-01-30 ; Gaps 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00661 ; Gaps 0;
 PRIOR FILING DATE: 2001-01-30 ; Gaps 0;
 PRIOR APPLICATION NUMBER: PCT/US01/00670 ; Gaps 0;

Qy	1 YTQC 4
Db	111 27 YTQC 30

Search completed: July 9, 2003, 12:17:59
 Job time : 21.25 secs

Query Match 83.9%; Score 26; DB 9; Length 68;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-05-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Rinnomax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 34561

LENGTH: 64

TYPE: PRT

ORGANISM: *Homo sapiens*

FEATURE:

OTHER INFORMATION: MAP TO AC004689.5
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 19
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 16
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14
 OTHER INFORMATION: EXPRESSED IN BTM74, SIGNAL = 13
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 15
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 12
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 14
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 11
 OTHER INFORMATION: SWISSPROT HIT: Q53176, EVALUE 1.90e+00
 US-09-864-761-34561

Query Match 83.9%; Score 26; DB 10; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQC 4
 Db 111
 52 YTQC 55

RESULT 15
 US-10-083-357-1024
 ; Sequence 1024, Application US/10083357
 ; Publication No. US20030054370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Qiangdong Zeng et al.
 ; TITLE OF INVENTION: Systemic discovery of New Genes
 ; FILE REFERENCE: 03296-090
 ; CURRENT APPLICATION NUMBER: US/10/083,357
 ; CURRENT FILING DATE: 2002-02-27

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ON protein - protein search, using sw model

Run on: July 9, 2003, 12:00:11 ; Search time 143.25 Seconds
 (without alignments)
 22.504 Million cell updates/sec

Title: US-09-851-058-3
 Perfect score: 31
 Sequence: 1 YTOCR 5

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending Patents_AA_Main:
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 27: /cgn2_6/ptodata/1/paa/US60_COMBO.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	100.0	39	19 US-09-513-996A-11153 Sequence 11153, A
2	31	100.0	155	21 US-09-791-537-10157 Sequence 101157, A
3	31	100.0	155	21 US-09-791-537-129198 Sequence 129198, A
4	31	100.0	155	21 US-09-791-537-129501 Sequence 129201, A
5	31	100.0	155	21 US-09-791-537-129589 Sequence 129589, A
6	31	100.0	157	21 US-09-791-537-53532 Sequence 53532, A

RESULT 1
 US-09-513-996A-11153
 Sequence 11153, Application US/09513996A
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
 FILE REFERENCE: 2750-709P
 CURRENT APPLICATION NUMBER: US/09/513, 996A
 CURRENT FILING DATE: 2000-07-25
 NUMBER OF SEQ ID NOS: 81028
 SEQ ID NO 11153
 LENGTH: 39
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE: NAME/KEY: UNSURE
 LOCATION: 1..39 /
 OTHER INFORMATION: any n or Xaa = unknown
 OTHER INFORMATION: Location 1..39 / Ceres Seq. ID 1035338
 US-09-513-996A-11153

Query Match Best Local Similarity Score: 31; DB: 19; Length: 39;
 Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YTOCR 5

Sequence 1947, AP
 Sequence 98, AP
 Sequence 99, AP
 Sequence 12740, A
 Sequence 3268, AP
 Sequence 3263, A
 Sequence 3964, AP
 Sequence 3964, AP
 Sequence 1135, AP
 Sequence 1139, AP
 Sequence 60526, A
 Sequence 190319, Sequence 10711, A
 Sequence 103013, Sequence 36108, A
 Sequence 9040, AP
 Sequence 114, AP
 Sequence 20509, A
 Sequence 16715, A
 Sequence 45035, A
 Sequence 36108, A
 Sequence 4107, AP
 Sequence 27566, A
 Sequence 27565, A
 Sequence 11481, A
 Sequence 77513, A
 Sequence 11513, A
 Sequence 9005, AP
 Sequence 10983, Sequence 143787,
 Sequence 143801,
 Sequence 43, AP1
 Sequence 55403, A
 Sequence 3846, AP
 Sequence 30714, A
 Sequence 30271, A
 Sequence 5678, A
 Sequence 665, AP
 Sequence 110137, Sequence 7312, AP

Db 14 YTOCR 18

RESULT 2

US-09-791-537-101157

Sequence 101157, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO: 101157

LENGTH: 155

TYPE: PRT

ORGANISM: Mus musculus

US-09-791-537-101157

Query Match

Best Local Similarity 100.0%; Score 31; DB 21; Length 155;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTOCR 5

Db 115 YTOCR 119

RESULT 3

US-09-791-537-129198

Sequence 129198, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO: 129589

LENGTH: 155

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-791-537-129589

Query Match

Best Local Similarity 100.0%; Score 31; DB 21; Length 155;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTOCR 5

Db 115 YTOCR 119

RESULT 4

US-09-791-537-129201

Sequence 129201, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO: 53532

LENGTH: 157

TYPE: PRT

ORGANISM: Crictetus griseus

US-09-791-537-53532

Query Match

Best Local Similarity 100.0%; Score 31; DB 21; Length 157;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTOCR 5

Db 117 YTOCR 121

RESULT 7
US-09-570-581A-1947
Sequence 1947, Application US/09570581A
; GENERAL INFORMATION:
; APPLICANT: Celles Inc.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-0875P
; CURRENT APPLICATION NUMBER: US/09/570, 581A
; NUMBER OF SEQ ID NOS: 1950
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1947
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-570-581A-1947

RESULT 8
US-09-573-655A-98
; Sequence 98, Application US/09573655A
; GENERAL INFORMATION:
; APPLICANT: SOLOV'EV, Victor and TROIKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573, 655A
; NUMBER OF SEQ ID NOS: 3280
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 98
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-573-655A-98

Query Match 100.0%; Score 31; DB 19; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
Db 194 YTQCR 198

RESULT 9
US-09-573-655B-98
; Sequence 98, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOV'EV, Victor and TROIKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573, 655B
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 98
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-573-655B-98

Query Match 100.0%; Score 31; DB 19; Length 378;
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
Db 194 YTQCR 198

RESULT 10
US-60-360-039-12740
; Sequence 12740, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkley, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 12740
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; US-60-360-039-12740

Query Match 100.0%; Score 31; DB 27; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
Db 282 YTQCR 286

RESULT 11
US-60-360-039-32688
; Sequence 3268, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkley, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 3268
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(676)
; OTHER INFORMATION: unsure at all Xaa locations
; US-60-360-039-32688

Query Match 100.0%; Score 31; DB 27; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
Db 300 YTQCR 304

RESULT 12
US-09-17-507-38263
; Sequence 38363, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WERNSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09417, 507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 38363
; LENGTH: 720
; TYPE: PRT
; ORGANISM: A. fumigatus
; US-09-417-507-38363

Query Match Best Local Similarity Score DB Length
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 246 YTECR 250

RESULT 13
PCT-US01-18569-3964
; Sequence 3964, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA13PCT
; CURRENT APPLICATION NUMBER: PC/TUS01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3964
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: A. fumigatus
; FEATURE:
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (34)

Query Match Best Local Similarity Score DB Length
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 246 YTECR 250

RESULT 14
US-10-264-049-3964
; Sequence 3964, Application US/10264049
; GENERAL INFORMATION:
; APPLICANT: BIRSE ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA13P1
; CURRENT APPLICATION NUMBER: US/10/264, 049

Query Match Best Local Similarity Score DB Length
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 25 YTECR 29

RESULT 15
US-60-42-896-1135
; Sequence 1135, Application US/60142896
; GENERAL INFORMATION:
; APPLICANT: Kerlavage, Anthony
; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000052
; CURRENT APPLICATION NUMBER: US/60/142,896
; CURRENT FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 1584
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1135
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Drosophila
; US-60-142-896-1135

Query Match Best Local Similarity Score DB Length
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 32 YTECR 36

Search completed: July 9, 2003, 12:13:18
Job time: 144.25 secs

GenCore version 5.1.6
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OM Protein - protein search, using sw model

Run on: July 9, 2003, 12:00:51 ; search time 47.25 Seconds
(without alignments)

27.740 Million cell updates/sec

Title: US-09-851-058-3

Perfect score: 31

Sequence: 1 YTQCR 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1221054 seqs, 262139423 residues

Total number of hits satisfying chosen parameters: 1221054

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Pending_Patents_AA_New.*
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMBO.pep:*
2: /cgn2_6/ptodata/1/paa/PCT_NEW_COMBO.pep:*
3: /cgn2_6/ptodata/1/paa/US06_NEW_COMBO.pep:*
4: /cgn2_6/ptodata/1/paa/US07_NEW_COMBO.pep:*
5: /cgn2_6/ptodata/1/paa/US07_NEW_COMBO.pep:*
6: /cgn2_6/ptodata/1/paa/US07_NEW_COMBO.pep:*
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8: /cgn2_6/ptodata/1/paa/US09_NEW_COMBO.pep:*
9: /cgn2_6/ptodata/1/paa/US09_NEW_COMBO.pep:*
10: /cgn2_6/ptodata/1/paa/US10_NEW_COMBO.pep:*
11: /cgn2_6/ptodata/1/paa/US10_NEW_COMBO.pep:*
12: /cgn2_6/ptodata/1/paa/US10_NEW_COMBO.pep:*
13: /cgn2_6/ptodata/1/paa/US60_NEW_COMBO.pep:*
14: /cgn2_6/ptodata/1/paa/US60_NEW_COMBO.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	100.0	5	PCT-US02-14369-3
2	31	100.0	5	US-09-851-058-3
3	31	100.0	155	US-10-219-051B-12561
4	31	100.0	155	US-10-219-051B-14320
5	31	100.0	372	US-10-437-963-157136
6	31	100.0	555	US-10-437-963-127740
7	31	100.0	676	US-10-369-493-3268
8	28	90.3	129	US-10-446-203-1071
9	28	90.3	304	US-10-282-122A-75073
10	28	90.3	304	US-10-282-122A-75073
11	28	90.3	304	US-10-282-122A-75073
12	28	90.3	313	US-10-437-963-177062
13	28	90.3	315	US-10-282-122A-59088
14	28	90.3	322	PCT-US02-3277-5811
15	28	90.3	322	US-09-978-825-5011
16	28	90.3	322	US-10-057-498-5011
17	28	90.3	401	US-10-369-493-4107
18	28	90.3	471	US-10-254-763-12
19	28	90.3	498	US-10-369-493-3846
20	28	90.3	513	PCT-US02-3277-29554
21	28	90.3	513	US-09-978-825-29554
22	28	90.3	818	US-10-156-761-19660
23	28	90.3	840	US-10-369-493-22262
24	28	90.3	856	US-10-282-122A-53654
25	27	87.1	5	PCT-US02-14369-2
26	27	87.1	10	US-09-851-058-2
27	27	87.1	9	US-10-394-980-139
28	27	87.1	9	US-10-394-980-365
29	27	87.1	40	PCT-US03-08715-27
30	27	87.1	41	US-10-437-963-140723
31	27	87.1	53	US-10-424-599-227392
32	27	87.1	60	US-10-424-599-145972
33	27	87.1	61	US-10-282-122A-52390
34	27	87.1	61	US-10-282-122A-58955
35	27	87.1	61	US-10-421-684-1388
36	27	87.1	67	US-10-437-963-140723
37	27	87.1	72	US-10-424-599-227392
38	27	87.1	87	US-10-219-382-2772
39	27	87.1	87	US-10-219-382A-2772
40	27	87.1	103	US-10-424-599-239127
41	27	87.1	107	US-10-26-17-60
42	27	87.1	108	US-10-424-599-229646
43	27	87.1	115	US-724-676A-63170
44	27	87.1	115	US-09-724-676A-63170
45	27	87.1	117	US-10-424-599-254138

ALIGNMENTS

RESULT 1				
PCT-US02-14369-3				
Sequence 3, Application PCT-US0214369				
GENERAL INFORMATION:				
APPLICANT: Parker, Kenneth				
APPLICANT: Nadler, Timothy				
APPLICANT: Abersold, Rudolf				
APPLICANT: Smolla, Marcus				
TITLE OF INVENTION: Process for Analyzing Protein Samples				
FILE REFERENCE: SYP-172				
CURRENT APPLICATION NUMBER: PCT-US02/14369				
NUMBER OF SEQ ID NOS: 3				
SOFTWARE: Patentin version 3.1				
SEQ ID NO 3				
LENGTH: 5				
TYPE: PRT				
FEATURE: OTHER INFORMATION: Synthetic peptides				
PCT-US02-14369-3				
Query Match Score 100.0%; Pred. No. 1.1e+06; Mismatches 0;				
Best Local Similarity 100.0%; Matches 5; Conservative 0; Indels 0; Gaps 0;				
QY 1 YTQCR 5				
Db 1 YTQCR 5				
RESULT 2				
US-09-851-058-3				
Sequence 3, Application PCT-US02-14369-3				
Sequence 3, Application PCT-US0214369				
GENERAL INFORMATION:				
APPLICANT: Parker, Kenneth				
APPLICANT: Nadler, Timothy				
APPLICANT: Abersold, Rudolf				
APPLICANT: Smolla, Marcus				
SEQUENCE 1				
Sequence 1, Application PCT-US0214369				
Sequence 1, Sequence 12561, A				
Sequence 1, Sequence 14320, A				
Sequence 1, Sequence 157136, A				
Sequence 1, Sequence 17240, A				
Sequence 2, Sequence 10711, A				
Sequence 2, Sequence 16164, A				
Sequence 2, Sequence 75073, A				
Sequence 3, Sequence 326B, AP				
Sequence 4, Sequence 17062, AP				
Sequence 5, Sequence 59088, A				
Sequence 6, Sequence 5811, AP				
Sequence 7, Sequence 5811, AP				
Sequence 8, Sequence 4071, AP				
Sequence 9, Sequence 12, AP				
Sequence 10, Sequence 3846, AP				

TITLE OF INVENTION: Process for Analyzing Protein Samples
 FILE REFERENCE: SVP-172
 CURRENT APPLICATION NUMBER: US/09/851,058
 CURRENT FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 3
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial sequence
 OTHER INFORMATION: Synthetic peptides
 ;
 US-09-851-058-3
 Query Match Best Local Similarity 100.0%; Score 31; DB 10; Length 5; Type: PRT
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 Db 1 YTQCR 5
 ;
 RESULT 3
 US-10-219-051B-12561
 Sequence 12561, Application US/10219051B
 ; GENERAL INFORMATION:
 ; APPLICANT: The General Hospital Corporation doing business as Massachusetts General Hospital / Bayer AG
 ; TITLE OF INVENTION: Nucleotide sequences involved in pain
 ; FILE REFERENCE: LEA 35693 Foreign Countries
 ; CURRENT APPLICATION NUMBER: US/10/219,051B
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: US 60/312,147
 ; PRIOR FILING DATE: 2001-08-14
 ; PRIOR APPLICATION NUMBER: US 60/346,382
 ; PRIOR FILING DATE: 2001-11-01
 ; PRIOR APPLICATION NUMBER: US 60/333,347
 ; NUMBER OF SEQ ID NOS: 14715
 ; SOFTWARE: Perl script
 ; SEQ ID NO 12561
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; DATABASE ACCESION NUMBER: SWISS-Prot / P77079
 ; PUBLICATION INFORMATION:
 ; DATABASE ENTRY DATE: 1998-07-15
 ;
 US-10-219-051B-12561
 Query Match Best Local Similarity 100.0%; Score 31; DB 12; Length 5; Type: PRT
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 Db 115 YTQCR 119
 ;
 RESULT 5
 US-10-437-963-157136
 Sequence 157136, Application US/10437963
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Babzuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 20-966
 ; SEQ ID NO 157136
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_56737C.1.pep
 ;
 US-10-437-963-157136
 Query Match Best Local Similarity 100.0%; Score 31; DB 12; Length 372; Type: PRT
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 Db 206 YTQCR 210
 ;
 RESULT 6
 US-10-369-493-12740
 Sequence 12740, Application US/10369493
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIORITY INFORMATION:
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 US-10-219-051B-14320
 Query Match Best Local Similarity 100.0%; Score 31; DB 12; Length 155; Type: PRT
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTQCR 5
 Db 115 YTQCR 119
 ;
 RESULT 4
 US-10-219-051B-14320
 Sequence 14320, Application US/10219051B
 ; GENERAL INFORMATION:
 ; APPLICANT: The General Hospital Corporation doing business as Massachusetts General Hospital / Bayer AG
 ; TITLE OF INVENTION: Nucleotide sequences involved in pain
 ; FILE REFERENCE: LEA 35693 Foreign Countries
 ; CURRENT APPLICATION NUMBER: US/10/219,051B
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: US 60/312,147
 ; PRIOR FILING DATE: 2001-08-14
 ; PRIOR APPLICATION NUMBER: US 60/346,382

PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 12740
 LENGTH: 555
 TYPE: PRT
 ORGANISM: *Aspergillus nidulans*
 US-10-369-493-12740

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
5;	100.0%	12	555	100.0%	2.3e+02	0	0	0	0
Conservative									
Matches									

Qy 1 YTQCR 5
 Db 282 YTQCR 286

RESULT 7
 US-10-369-493-3268
 Sequence 3208, Application US/10369493
 GENERAL INFORMATION:
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 3268
 LENGTH: 676
 TYPE: PRT
 ORGANISM: *Neurospora crassa*
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(676)
 OTHER INFORMATION: unsure at all xaa locations

US-10-369-493-3268

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
5;	100.0%	12	676	100.0%	2.6e+02	0	0	0	0
Conservative									
Matches									

Qy 1 YTQCR 5
 Db 300 YTQCR 304

RESULT 8
 US-10-446-203-10711
 Sequence 10711, Application US/10446203
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 FILE REFERENCE: 2709 2004001
 CURRENT APPLICATION NUMBER: US/10/446,203
 CURRENT FILING DATE: 2003-05-27
 PRIOR APPLICATION NUMBER: US/09/489,039
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 10711
 LENGTH: 129
 TYPE: PRT
 ORGANISM: *Klebsiella pneumoniae*
 US-10-446-203-10711

RESULT 9
 US-10-282-122A-73614
 Sequence 73614, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Travick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-05-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-03-16
 Remaining prior Application data removed - See file wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 73614
 LENGTH: 304
 TYPE: PRT
 ORGANISM: *Salmonella paratyphi A*
 US-10-282-122A-73614

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
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Conservative									
Matches									

Qy 1 YTQCR 5
 Db 167 YTQCR 171

RESULT 10
 US-10-282-122A-75073
 Sequence 75073, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 US-10-446-203-10711

APPLICANT: Zamudio, Carlos ; PRIORITY APPLICATION NUMBER: 60/191,078
 APPLICANT: Malone, Cheryl ; PRIORITY FILING DATE: 2000-03-21
 APPLICANT: Haselbeck, Robert ; PRIORITY APPLICATION NUMBER: 60/206,848
 APPLICANT: Ohlsen, Kari ; PRIORITY FILING DATE: 2000-05-23
 APPLICANT: Zyskind, Judith ; PRIORITY APPLICATION NUMBER: 60/207,727
 APPLICANT: Wall, Daniel ; PRIORITY FILING DATE: 2000-05-26
 APPLICANT: Trawick, John ; PRIORITY APPLICATION NUMBER: 60/230,335
 APPLICANT: Carr, Grant ; PRIORITY FILING DATE: 2000-09-05
 APPLICANT: Yamamoto, Robert ; PRIORITY APPLICATION NUMBER: 60/230,347
 APPLICANT: Forsyth, R. ; PRIORITY FILING DATE: 2000-09-09
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/267,636
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 75073
 LENGTH: 304
 TYPE: PRT
 ORGANISM: Salmonella typhimurium
 -10-282-122A-75073
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 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/259,308
 PRIOR FILING DATE: 2000-12-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2000-10-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/267,636
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 75073
 LENGTH: 304
 TYPE: PRT
 ORGANISM: Salmonella typhi
 US-10-282-122A-75805
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 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YTOCR 5
 Db 167 YTOCK 171
 RESULT 12
 US-10-437-963-177062
 ; Sequence 177062, Application US/10437963
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbuzuk, Brad
 ; APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 177062
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_74751C.1.pep
 US-10-437-963-177062
 Query Match 90.3%; Score 28; DB 12; Length 313;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YTOCR 5
 Db 195 YTECR 200

RESULT 13
 US-10-282-122A-59088
 Sequence 59088, Application US/10282122A
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA-034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIORITY APPLICATION NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848
 PRIORITY FILING DATE: 2000-03-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-03-26
 PRIORITY APPLICATION NUMBER: 60/230,347
 PRIORITY FILING DATE: 2000-03-09
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-23
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/267,636
 PRIORITY FILING DATE: 2001-02-09
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 7814
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 59088
 LENGTH: 315
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-10-282-122A-59088

Query Match 90.3%; Score 28; DB 12; Length 315;
 Best Local Similarity 80.0%; Pred. No. 5.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTOCR 5
 Db 167 YTOCK 171

RESULT 14
 PCT-0502-32727-5811
 Sequence 5811, Application PC/TUS0232727
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer
 APPLICANT: Skeiky, Yasir
 APPLICANT: Persing, David
 APPLICANT: Bhattacharya, Ajay
 APPLICANT: Maisonneuve, Jean Francois
 APPLICANT: Zhang, Yanni
 APPLICANT: Wang, Siqing
 APPLICANT: Jen, Shyian
 APPLICANT: Lodes, Michael
 APPLICANT: Benson, Darin
 APPLICANT: Jones, Robert
 APPLICANT: Carter, Darick
 APPLICANT: Barth, Brenda
 APPLICANT: Doublass, John
 TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 FILE REFERENCE: 210121.514C1
 CURRENT APPLICATION NUMBER: US/09/978,825
 CURRENT FILING DATE: 2003-01-29
 NUMBER OF SEQ ID NOS: 30992
 SEQ ID NO 5811
 LENGTH: 322
 TYPE: PRT
 ORGANISM: Propioni acnes
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (262)
 OTHER INFORMATION: xaa = Any Amino Acid

US-09-978-825-5811

Query Match 90.3%; Score 28; DB 10; Length 322;
 Best Local Similarity 80.0%; Pred. No. 6.5e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTOCR 5
 Db 148 YTECR 152

Search completed: July 9, 2003, 12:16:33
 Job time : 48.25 secs

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A;Accession: PG6042
A;Molecule type: protein
A;Residues: 52-77;38-150 <IAR2>
C;Genetics:
A;Gene: near-2
C;Superfamily: pancreatic ribonuclease
C;Keywords: bone; disulfide bond; glycoprotein; hydrolase; RNA binding
F;-27/Domain: signal sequence #status predicted
F;28-156/Product: eosinophil-associated ribonuclease 2 #status predicted <SIG>
F;38-62-151/active site: HIS LYS HIS #status predicted
F;47-106 61-19 79-134 86-94/Disulfide bonds: #status predicted
F;89-96,107/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match Best Local Similarity 100.0%; Score 31; DB 2; Length 156;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 116 YTQCR 120

RESULT 3
BB5059
hypothetical protein AT4904690 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: BB5059
R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: BB5059
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: GB:NC_001268; NID:97267227; PIDN:CAB80834.1; CSPDB:GN00140
A;Gene: AT4904690
A;Map position: 4

Query Match Best Local Similarity 100.0%; Score 31; DB 2; Length 378;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 194 YTQCR 198

RESULT 4
AF0730
probable membrane protein Sru2000 [imported] - *Salmonella enterica* subsp. *enterica* serovar
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0730
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
rson, J.D.; Sodow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.-P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A;Reference number: A64300; MUID:96337990; PMID:8888087
A;Accession: D64512
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-432 <BUL>
A;Cross-references: GB:L77118; NID:91500644; TIGR:MJECL21; PIDN:AMC37092.1; PID:91522
C;Genetics:
A;Map position: ECREV24593-23295
A;Gene: plasmid
A;Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachrom
C;Superfamily: Methanococcus jannaschii plasmid PURB800 hypothetical protein MJECL21
Query Match Best Local Similarity 90.3%; Score 28; DB 2; Length 432;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 299 YTQCR 303

RESULT 5
FB1348
ABC Transport system ATP-binding protein Cj0774c [imported] - *Campylobacter jejuni* (s
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: F81348
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar
Nature 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
A;Reference number: A81250; MUID:20150912; PMID:10686204
A;Accession: F81348
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <PAR>
A;Cross-references: GB:AL1139076; GB:AL111168; NID:96968128; PIDN:CAB73039.1; PID:9696
A;Experimental source: serotype 02, strain NCTC 1168
C;Genetics:
A;Gene: CJ0774c
C;Superfamily: probable ABC-type transport protein abc; ATP-binding cassette homology
Query Match Best Local Similarity 90.3%; Score 28; DB 2; Length 336;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 110 YTQCK 114

RESULT 6
D64512
hypothetical protein MJECL21 - *Methanococcus jannaschii* plasmid PURB800
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000
C;Accession: D64512
R;Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.G.; Meirick, J.M.; Glodek,
Reich, C.I.; Overbeek, R.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.-P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A;Reference number: A64300; MUID:96337990; PMID:8888087
A;Accession: D64512
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-432 <BUL>
A;Cross-references: GB:L77118; NID:91500644; TIGR:MJECL21; PIDN:AMC37092.1; PID:91522
C;Genetics:
A;Map position: ECREV24593-23295
A;Gene: plasmid
A;Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachrom
C;Superfamily: *Methanococcus jannaschii* plasmid PURB800 hypothetical protein MJECL21
Query Match Best Local Similarity 90.3%; Score 28; DB 2; Length 432;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTQCR 5
Db 299 YTQCR 303

tryptophanase VCA0161 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: B82492
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwynn, M.L.; Dodson, R.J.; chardson, D.; Brzuska, M.D.; Vanatharan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*. A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: B82492
A;Map position: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <HEI>
A;Cross-references: GB:AB004357; GB:AE003853; NID:99657547; PIDN:AAF96074.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:
A;Gene: VCA0161
A;Map position: 2
C;Superfamily: tryptophanase

Query Match	Score 28;	DB 2;	Length 472;
Best Local Similarity 80.0%;	Pred. No. 2e+02;	1; Mismatches 0;	Indels 0;
Matches 4;	Conservative		Gaps 0;

QY 1 YTOCR 5
||:||
Db 291 YTECR 295

RESULT 8

tryptophanase (EC 4.1.99.1) - *Escherichia coli* (strain K-12)

C;Species: *Escherichia coli*
C;Date: 14-Nov-1983 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002

C;Accession: E015173; A91189; I41097; I509358; A01136
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: E05173
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-476 <BLAT>
A;Cross-references: GB:AB000448; GB:U00096; NID:91790142; PIDN:AACT6731.1; PID:91790144;
A;Experimental source: strain K-12, substrain MG1655
R;Deeley, M.C.; Yanofsky, C.
J. Bacteriol. 147, 787-796, 1981

A;Title: Nucleotide sequence of the structural gene for tryptophanase of *Escherichia coli*
A;Reference number: A91789; MUID:82007678; PMID:6268608

A;Molecule type: DNA
A;Residues: 6-141, 'T', 143, 'QG', 146-383, 'TG', 386-476 <DEEE>
A;Note: the authors translated the codons GAT, ACG, and CAG for residues 142, 144, and 146. R;Kagamiyama, H.; Matsubara, H.; Snell, E.E.
J. Biol. Chem. 247, 1576-1586, 1972

A;Title: The chemical structure of tryptophanase from *Escherichia coli*. III. Isolation and characterization of the tryptophanase from *Escherichia coli*. R;Tokushige, M.; Tsujimoto, N.; Oda, T.; Honda, T.; Yumoto, N.; Ito, S.; Yamamoto, M.; Biichimie 71, 711-720, 1989

A;Title: Role of cysteine residues in tryptophanase for monovalent cation-induced activation R;Stewart, V.J.; Yanofsky, C.
A;Reference number: I41097; MUID:8932326; PMID:2502187

A;Accession: I41097
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 6-303, 'TG', 386-476 <RES>
A;Cross-references: EMBL:X15974; NID:941935; PIDN:CAA34096.1; PID:941936
R;Stewart, V.J.; Yanofsky, C.
J. Bacteriol. 164, 731-740, 1985

RESULT 9

tryptophanase [imported] - *Escherichia coli* (strain 0157:H7, substrain RIMD 0509952)

C;Species: *Escherichia coli*
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C;Accession: E91209
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, R.; Ishii, K.; Yokoyama, K.; Han, C. DNA Res. B, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7 and 9 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91209
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <HEI>
A;Cross-references: GB:BA000007; PIDN:BA038068.1; PID:913364120; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: E9s4645
C;Superfamily: tryptophanase

Query Match	Score 28;	DB 2;	Length 476;
Best Local Similarity 80.0%;	Pred. No. 2e+02;	1; Mismatches 0;	Indels 0;
Matches 4;	Conservative		Gaps 0;

QY 1 YTOCR 5
||:||
Db 296 YTECR 300

RESULT 10

tryptophanase [imported] - *Escherichia coli* (strain 0157:H7, substrain EDL933)

C;Species: *Escherichia coli*
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: H86055
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May R.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H86055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <STO>
A;Cross-references: GB:AB005174; NID:912518553; PIDN:AG58908.1; GSPDB:GN00145; UWGP: C;Genetics:

A;Gene: tnaA
C;Superfamily: tryptophanase
F;599-632/Domain: tetratricopeptide repeat homology <TT5>
Query Match 90.3%; Score 28; DB 2; Length 476;
Best Local Similarity 80.0%; Pred. No. 2e+02; 1; Mismatches
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTOCR 5
Db 296 YTECR 300

RESULT 11
T35872
DNA gyrase-like protein - *Streptomyces coelicolor*
C;Species: *Streptomyces coelicolor*
C;Accession: T35872
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: 221592
A;Accession: T35872
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-818 <OLI>
A;Cross-references: EMBL:AL009204; PIDN:CAA15793.1; GSPDB:GN00070; SCOEDB:SCB910.03C
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCB910.03C
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (ATP-hydrolyzing) chain A; yeast (Saccharomyces cerevisiae)

Query Match 90.3%; Score 28; DB 2; Length 818;
Best Local Similarity 80.0%; Pred. No. 3.1e+02; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTOCR 5
Db 134 YTECR 138

RESULT 12
A27832
Cell division control protein Cdc16 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL02c
C;Species: *Saccharomyces cerevisiae*
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 11-Jan-2000
C;Accession: A27832; S57839
R;Icho, T.; Wickner, R.B.
A;Title: Metal-binding nucleic acid-binding finger sequences in the CDC16 gene of *Sacch*
A;Nucleic Acids Res. 15, 8439-8450, 1987
A;Accession: A27832; MUID:88040465; PMID:283230
A;Molecule type: DNA
A;Residues: 1-840 <ICH>
A;Cross-references: EMBL:X06155; NID:93477; PIDN:CAA29521.1; PID:93478
R;Rieger, M.
A;Reference number: S37832
A;Accession: S37832
A;Molecule type: DNA
A;Residues: 1-840 <RIES>
A;Cross-references: EMBL:228022; NID:9486014; PIDN:CAA81857.1; PID:9486015; MIPS:YKL022c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:CDCC16
A;Cross-references: SGD:S0001505; MIPS:YKL022c
A;Map position: III:
C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat hc
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:CDCC16
A;Cross-references: SGD:S0001505; MIPS:YKL022c
A;Map position: III:
C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat hc
C;Keywords: isomerase
F;599-632/Domain: tetratricopeptide repeat homology <TT5>
F;633-665/Domain: tetratricopeptide repeat homology <TT6>
Query Match 90.3%; Score 28; DB 2; Length 902;
Best Local Similarity 80.0%; Pred. No. 3.3e+02; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTOCR 5
Db 106 YTECR 110

RESULT 13
AB1914
DNA gyrase A chain [imported] - *Nostoc* sp. (strain PCC 7120)
C;Species: *Nostoc* sp. strain PCC 7120
A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C;Accession: AB1914
R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku
Nakazaki, N.; Shinjo, S.; Sugimoto, M.; Takizawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21555285; PMID:11759840
A;accession: AB1914
A;Species: *Nostoc* sp.
A;Molecule type: DNA
A;Residues: 1-872 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72817.1; PID:917130205; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: AB10860
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomeras
Query Match 90.3%; Score 28; DB 2; Length 872;
Best Local Similarity 80.0%; Pred. No. 3.3e+02; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTOCR 5
Db 122 YTECR 126

RESULT 14
AF3362
DNA topoisomerase (ATP-hydrolysing) (EC 5.99.1.3) chain A [imported] - *Brucella melit*
C;Species: *Brucella melitensis*
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C;Accession: AF3362
R;DelVecchio, V.G.; Kaparthy, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hugus, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*
A;Reference number: AD3252; PMID:11756688
A;Accession: AF3362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-902 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52065.1; PID:917982834; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BM10884
A;Map position: I
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomeras
C;Keywords: isomerase
F;599-632/Domain: tetratricopeptide repeat homology <TT1>
F;497-530/Domain: tetratricopeptide repeat homology <TT2>
F;531-564/Domain: tetratricopeptide repeat homology <TT3>
F;565-598/Domain: tetratricopeptide repeat homology <TT4>

RESULT 15

AB2762

DNA gyrase subunit A [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C;Accession: AB2762

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:1743193

A;Accession: AB2762

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-906 <KUR>

A;Cross-references: GB:AB008688; PIDN:AAL42512.1; PID:917739931; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: gyrA

A;Map position: circular chromosome

C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase

Query Match 90.3%; Score 28; DB 2; Length 906;

Best Local Similarity 80.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
||:||
Db 106 YTECR 110

Search completed: July 9, 2003, 12:02:46
Job time : 10.25 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 11:55:50 ; Search time 7.75 Seconds
(without alignments)
26.759 Million cell updates/sec

Title: US-09-851-058-3

Perfect score: 31
Sequence: 1 YIQCR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	31	100.0	155	1 ECP1_MOUSE	P97426 mus musculus
2	31	100.0	155	1 ECP1_RAT	P70709 rattus norvegicus
3	31	100.0	156	1 ECP2_MOUSE	P97425 mus musculus
4	31	100.0	156	1 ECP3_MOUSE	035290 mus musculus
5	28	90.3	304	1 PAGO_SALTY	030646 salmonella
6	28	90.3	432	1 Y221_METJA	060281 methanococcus
7	28	90.3	471	1 TNA1_ECOLI	08xb34 escherichia
8	28	90.3	471	1 TNA1_ECOLI	00913 escherichia
9	28	90.3	472	1 TNA1_VIBCH	09kn05 virio cholerae
10	28	90.3	840	1 C016_YEAR	P09798 saccharomyces cerevisiae
11	27	87.1	61	1 RS14_CLOPE	08xht6 clostridium
12	27	87.1	61	1 RS14_HELPPJ	09zjs5 helicobacte
13	27	87.1	61	1 RS14_HELPPJ	P56021 helicobacter
14	27	87.1	89	1 ITI2_ARATH	042328 arabidopsis
15	27	87.1	89	1 ITI3_ARATH	022865 arabidopsis thaliana
16	27	87.1	99	1 ITI1_SINEL	P26780 snapdragon
17	27	87.1	122	1 RBS2_HDMR	Q59461 hydrogenase
18	27	87.1	210	1 PSBP_PORPU	P50472 porphyra purpurea
19	27	87.1	251	1 HYBA_FUGRR	013074 fugu rubripinnis
20	27	87.1	342	1 CRIB_STRRGR	P54977 streptomyces
21	27	87.1	347	1 CHML_CHICK	09ppub gallus gallus
22	27	87.1	451	1 IJK1_CAVPO	P57044 cavia porcellus
23	27	87.1	452	1 IJK1_HUMAN	P013418 homo sapiens
24	27	87.1	452	1 IJK2_HUMAN	P57043 homo sapiens
25	27	87.1	452	1 IJK_MOUSE	055222 mus musculus
26	27	87.1	717	1 MTO1_HUMAN	09yyzz2 homo sapiens
27	87.1	729	1 CULG_CAEEL	021346 caenorhabditis elegans	
28	87.1	1122	1 TERT_MOUSE	070372 mus musculus	
29	83.9	64	1 RL35_URBPA	09ppqr3 ureaplasma	
30	83.9	84	1 RNS_GIRCA	029535 giraffa camelopardalis	
31	83.9	87	1 RL37_SCCHA	044125 schistosoma haematobium	
32	83.9	100	1 YJF0_YEAST	P470045 yeast	
33	83.9	145	1 Y586_HAEIN	P44019 haemophilus suis	

ALIGNMENTS

RESULT 1	ECP1_MOUSE	ID	ECP1_MOUSE	STANDARD:	PRT:	155 AA.
		ID	P97426	AC	P97426;	
		DT	01-NOV-1997	(Rel.	35,	Created)
		DT	01-NOV-1997	(Rel.	35,	Last sequence update)
		DT	15-DEC-1998	(Rel.	37,	Last annotation update)
		DE	Bosinophil cationic protein 1 precursor (EC 3.1.27.-)	(ECP 1)	DE	(Ribonuclease 3-1) (RNase 3-1) (Bosinophil secondary granule ribonuclease-1) (EAR-1).
		DE			GN	EARL.
		OS	Mus musculus (Mouse)		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
		OX			NCBI_TAXID=10090;	
		RP	[1]			
		RC	SEQUENCE FROM N.A.			
		RC	STRAIN=C57BL/6J;			
		RX	MEDLINE=9705749; PubMed=8901588;			
		RA	Larson K.A., Olson E.V., Madden B.J., Gleich G.J., Lee N.A., Lee J.J.:			
		RT	"Two highly homologous ribonucleases genes expressed in mouse eosinophils identify a larger subgroup of the mammalian ribonuclease superfamily."			
		RT	superfamily.", acid. sci. U.S.A. 93:12370-12375(1996).			
		RL	Proc. Natl. Acad. Sci. U.S.A. 93:12370-12375(1996).			
		CC	possesses a wide variety of biological activities (by similarity).			
		CC	-!- FUNCTION: CYTOTOXIN AND HELMINTOTOXIN WITH RIBONUCLEASE ACTIVITY.			
		CC	-!- SUBCELLULAR LOCATION: MATRIX OF EOSINOPHIL'S LARGE SPECIFIC GRANULE (BY SIMILARITY).			
		CC	-!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
		CC				
		DR	EMBL: U72032; ARB3786.1; -.			
		DR	HSSP: P00556; 2RNS.			
		DR	MGD: MGI:108021; Earl.			
		DR	InterPro: IPR001427; RNaseA.			
		DR	IntePro: IPR001427; RNaseA.			
		Pfam	PF00074; rnasek; 1.			
		DR	PRINTS: PR00794; RIBONUCLEASE.			
		DR	PRODOM: PD00555; RNase; 1.			
		DR	SMART: SM00922; RNASE_Pc; 1.			
		DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
		KW	Hydrolyase; Nuclease; Endonuclease; Endonuclease; Bosinophil; Toxin; Glycoprotein; Signal.			
		FT	1	25		POTENTIAL.
		FT	VHBL_PMY			BOSINOPHIL CATIONIC PROTEIN 1.
		FT	ACT_SITE	155		
		FT	ACT_SITE	38		BY SIMILARITY.
		FT	ACT_SITE	62		BY SIMILARITY.
		FT	ACT_SITE	150		BY SIMILARITY.
		FT	DISUFDID	106		BY SIMILARITY.
		FT		118		

Y221_METJA STANDARD; PRT; 432 AA.
 ID Y221_METJA
 AC Q60381;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJECI21.
 RA MJECI21.
 OS Methanococcus Jannaschii.
 OC Archaea; Buryarchaeota; Methanococcaceae; Methanococcales;
 OX NCBI_TAXID=2190;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; Published=8688087;
 RA Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blattner J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Karlaage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirnness E.F., Weinstock G.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hama M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Keane B.P., Borodovsky M.,
 RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.;
 PRT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii."; PDB 1MJC; PDB 1MJD; PDB 1MJE; PDB 1MJC_A; PDB 1MJC_B;
 CC Science 273:1050-1073(1996).
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 or send an email to license@isb-sib.ch).
 DR EMBL; L77118; AAC37092.1; -;
 DR TIGR; MJECI21; -;
 DR DR "Hypothetical protein: Complete proteome."
 SQ SEQUENCE 432 AA; 51081 MW; DBADEF205C43A4F90 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 432;
 Best Local Similarity 80.0%; Pred. No. 69;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YTCR 5
 |||||
 Db 299 YTECR 303

RESULT 7
 ID TNAA_ECO57 STANDARD; PRT; 471 AA.
 AC ID TNAA_ECO57
 DT 08X034;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRYPTOPHANASE (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).
 TNAA OR Z503 OR RCS4445.
 OS Escherichia coli 0157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TAXID=83334;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=2007678; PubMed=6268608;
 RA Deley M.C., Yanofsky C.;
 RA "Nucleotide sequence of the structural gene for tryptophanase of
 Escherichia coli K-12"; J. Bacteriol. 147:787-796(1981).
 RN [2]
 SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.
 RC STRAIN=B177A;
 RX MEDLINE=8932226; PubMed=2502187;
 RA Tokushige M., Tsujimoto N., Oda T., Honda T., Yamoto N., Ito S.,

RESULT 8
 ID TNAA_ECOLI STANDARD; PRT; 471 AA.
 AC ID TNAA_ECOLI
 DT P00913; P8123;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRYPTOPHANASE (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase).
 TNAA OR IND OR B3708.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TAXID=562;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=2007678; PubMed=6268608;
 RA Deley M.C., Yanofsky C.;
 RA "Nucleotide sequence of the structural gene for tryptophanase of
 Escherichia coli K-12"; J. Bacteriol. 147:787-796(1981).
 RN [2]
 SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.
 RC STRAIN=B177A;
 RX MEDLINE=8932226; PubMed=2502187;
 RA Tokushige M., Tsujimoto N., Oda T., Honda T., Yamoto N., Ito S.,

RA YAMAMOTO M., Kim E.H., Hiragi Y.;
 RT Role of cysteine residues in tryptophanase for monovalent cation-
 RT induced activation.;
 RL Biochimie 71:711-720(1989).
 RN [3]
 SEQUENCE FROM N.A.
 RP STRAIN=K12 / MG1655;
 RX MEDLINE=93315143; PubMed=7686882;
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
 RT *DNA sequence and analysis of 136 kilobases of the *Escherichia coli*
 genome: organizational symmetry around the origin of replication.*;
 RT genomics 16:551-561(1993).
 RL [4]
 SEQUENCE OF TRYPTIC PEPTIDES.
 RC STRAIN=K12;
 RX MEDLINE=72134434; PubMed=4551944;
 RA Kagamiya H., Matsunara H., Snell E.E.;
 RT "The chemical structure of tryptophanase from *Escherichia coli*. 3.
 RT Isolation and amino acid sequence of the tryptic peptides.";
 RL J. Biol. Chem. 247:1576-1586(1972).
 RN [5]
 SEQUENCE OF 1-21 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=85033634; PubMed=3902796;
 RA Stewart V., Yanofsky C.;
 RT "Evidence for transcription antitermination control of tryptophanase
 operon expression in *Escherichia coli* K-12.";
 RL J. Bacteriol. 164:731-740(1985).
 RN [6]
 SEQUENCE OF 463-471 FROM N.A.
 RX MEDLINE=91216998; PubMed=2022620;
 RA Sarsero J.P., Wooley P.J., Golnick P.D., Yanofsky C., Pittard A.J.;
 RT "A new family of integral membrane proteins involved in transport of
 aromatic amino acids in *Escherichia coli*.";
 RL J. Bacteriol. 173:3231-3234(1991).
 RN [7]
 SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RX MEDLINE=9443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [8]
 RP MUTAGENESIS OF CYS-294 AND CYS-298.
 RX MEDLINE=8927810; PubMed=2659590;
 RA Phillips R.S., Golnick P.D.;
 RT "Evidence that cysteine 298 is in the active site of tryptophan
 indole-lyase.";
 RL J. Biol. Chem. 264:10627-10632(1989).
 CC -I CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
 CC -I COFACTOR: Pyridoxal phosphate.
 CC -I PATHWAY: Tryptophan catabolism.
 CC -I SUBUNIT: Homotetramer.
 CC -I SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
 CC
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 DR EMBL; K0032; AAA24676.1; -;
 DR EMBL; X15934; CA34056.1; -;
 DR EMBL; M11930; AA24679.1; -;
 DR EMBL; M59314; -; NOT_ANNOTATED_CDS.
 DR EMBL; L10328; AA62059.1; ALT_INIT.
 DR EMBL; AE004448; AAC76731.1; ALT_INIT.
 DR PIR; A01136; WZEC.
 DR HSSP; P28796; IAX4.

DR ECOBASE; G046_5, 6TH EDITION.
 DR Ecogene; EG1005; tRNA.
 DR InterPro; IPR001597; Beta_elim_lyase.
 DR Pfam; PF01212; Beta_elim_lyase; 1.
 DR ProdDB; PDO5927; Beta_elim_lyase; 1.
 DR PROSITE; PS00833; BETA_ELIM_LYASE; 1.
 KW Tryptophan catabolism; Lyase; Pyridoxal phosphate; Complete proteome.
 FT BINDING 270 270 PYRIDOXAL PHOSPHATE.
 FT MUTAGEN 294 294 C->S: IDENTICAL TO WT&-TYPE.
 FT MUTAGEN 298 298 C->S: ALTERED ACTIVITY.
 FT CONFLICT 137 140 DTQ->TTQG (IN REF. 1).
 FT CONFLICT 379 380 QA->TG (IN REF. 1 AND 2).
 SQ SEQUENCE 471 AA; 52773 MW; 5ACF1F41BD9D0034 CRC64;

Query	Match	Similarity	Score	DB	Length
Best Local	Local	80.0%	28	1	471
Matches	Similarity	Pred. No.			
4	Conservative	75			
OY	1	YTCR 5			
	:				
Db	291	YTECR 295			

RESULT 9

TNAA_VIBCH TNAA_VIBCH STANDARD; PRT; 472 AA.

ID TNAA_VIBCH ID TNAA_VIBCH ID TNAA_VIBCH ID TNAA_VIBCH
 RX MEDLINE=2046833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickley E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 cholerae.";
 RL Nature 406:477-483(2000).
 RN [2]
 SEQUENCE OF 51-241 FROM N.A.

RP STRAIN=Bengal; Tang T.H., Ravichandran M., Johari M.R., Zainuddin Z.F.;
 RA Tang T.H., Ravichandran M., Johari M.R., Zainuddin Z.F.;
 RT "Vibrio cholerae putative tryptophanase gene partial cds.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -I CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +
 CC NH(3).
 CC -I COFACTOR: Pyridoxal phosphate (By similarity).
 CC -I PATHWAY: Tryptophan catabolism.
 CC -I SUBUNIT: Homotetramer (By similarity).
 CC -I SIMILARITY: BELONGS TO THE BETA-ELIMINATING LYASE FAMILY.
 CC
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 CC
 DR EMBL; AE004357; AAC95074.1; -;
 DR EMBL; AF081274; AAC3284.1; -;
 DR HSSP; P28796; IAX4.

DR TIGR; VCA0161; -;
 DR InterPro; IPR001597; Beta_elm_lyase.
 DR Pfam; PF01212; Beta_elm_lyase; 1.
 DR PRODOM; PDB05927; Beta_elm_lyase; 1.
 DR PROTEB; PS00833; Beta_ELM_LYASE; 1.
 KW TRYPTOPHAN CATABOLISM; Lyase; Pyridoxal phosphate; Complete proteome.
 FT BINDING 270 270 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 472 AA; 52920 MW; 632384FS4C06FB7B9 CRC64;

Query Match	Best Local Similarity	Score	DB	Length
OY 1 YTCR 5	90.3%	28	1	472
Db 291 YTECR 295	80.0%	pred. No.	75	

RESULTS 10

ID	CC16_YEAST	STANDARD;	PRT;	840 AA.
AC	P09198;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DE	Cell division control protein 16.			
GN	CDC16 OR KL022C.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OX	NEBI_TAXID=4932;			
RN	[1]			
RP	SEQUENCE FROM N_A.			
RC	SPRAINER,B,WICKNER 1385;			
RX	MEDLINE-BB800465; PubMed=2823230;			
RA	Icho T., Wickner R.B.;			
RT	"Metal-binding, nucleic acid-binding finger sequences in the CDC16 gene of <i>Saccharomyces cerevisiae</i> ";			
RL	Nucleic Acids Res. 15:8439-8450(1987).			
RN	[2]			
RP	SEQUENCE FROM N_A.			
RA	Rieger M.;			
RL	Submitted (MAR-1994) to the EMBL/GenBank/DBJ/GenBank databases.			
RN	[3]			
RP	TPR REPEATS.			
RX	MEDLINE=90124639; PubMed=2404612;			
RA	Sikorski R.S., Boguski M.S., Goebel M., Hietter P.A.;			
RT	"A repeating amino acid motif in CDC23 defines a family of proteins and a new relationship among genes required for mitosis and RNA Cell 60:307-317(1990).			
RL	[4]			
RP	SUBUNITS.			
RX	MEDLINE=95009933; PubMed=7925276;			
RA	Lamb J.R., Michaud W.A., Sikorski R.S., Hietter P.A.;			
RT	"Cdc16P, Cdc27P and Cdc27P form a complex essential for mitosis.";			
RL	EMBO J. 13:4321-4328(1994).			
-!- FUNCTION: EXACT FUNCTION NOT KNOWN. REQUIRED FOR CHROMOSOME SEGREGATION. MUTATIONS IN CDC16 CAUSE CELLS TO ARREST UNIFORMLY AT G2/M AFTER DNA REPLICATION BUT PRIOR TO MITOTIC SPINDLE ELONGATION.				
-!- SUBUNIT: Cdc16, Cdc23 AND Cdc27 FORMS A MACROMOLECULAR COMPLEX.				
-!- SUBCELLULAR LOCATION: NUCLEAR.				
-!- SIMILARITY: CONTAINS 10 TPR REPEATS.				
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CC DR EMBL; X06165; CAA29521.1; -.				
CC DR EMBL; Z28022; CA81857.1; -.				
CC DR PIR; A27832; A27832.				
CC DR SGD; S0001505; CDC16.				
CC DR InterPro; IPR001440; TPR.				
CC DR Pfam; PF00515; TPR; 7.				
CC DR SMART; SM00028; TPR; 6.				
CC KW Nuclear protein.				
CC FT REPEAT 263 295 "TPR 1."				
CC FT REPEAT 296 329 TPR 2.				
CC FT REPEAT 359 392 TPR 3.				
CC FT REPEAT 497 530 TPR 4.				
CC FT REPEAT 531 564 TPR 5.				
CC FT REPEAT 565 598 TPR 6.				
CC FT REPEAT 599 632 TPR 7.				
CC FT REPEAT 633 666 TPR 8.				
CC FT REPEAT 674 707 TPR 9.				
CC FT REPEAT 708 741 TPR 10.				
CC SQ SEQUENCE 840 AA; 94991 MW; A096B3441083488 CRC64;				
Query Match	90.3%	Score	28	DB 1; Length 840;
OY 1 YTCR 5	80.0%	Pred. No.	1.28+02;	
Db 474 YTOCK 478	1;	Mismatches	0;	
RESULTS 11				
ID	RS14_CLOPE	STANDARD;	PRT;	61 AA.
AC	QBXIT6;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
RL	30S ribosomal protein S14.			
GN	RPSN OR CPE2392.			
OS	Clostridium perfringens.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OX	Clostridium.			
RN	NEBI_TAXID=1502;			
RN	[1]			
RP	SEQUENCE FROM N_A.			
RX	SPRAINER13 / Type A;			
RA	PubMed=11792842;			
RT	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kubara S., Hayashi H.; "Complete genome sequence of <i>Clostridium perfringens</i> , an anaerobic flesh-eater.".			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).			
CC	-!- FUNCTION: Known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site (BY similarity).			
CC	-!- FUNCTION: Known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site (BY similarity).			
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CC	EMBL; AP003194; BAB8208.1; -.			
CC	DR InterPro; IPR001209; Ribosomal S14.			
CC	DR Pfam; PF00255; Ribosomal S14; 1.			
CC	DR PROTEIN; PS00527; RIBOSOMAL_S14; 1.			
CC	Ribosomal Protein; Complete Proteome.			
SQ SEQUENCE 61 AA; 7280 MW; C3910B3227493E75 CRC64;				

Query Match

87.1%; Score 27; DB 1; Length 61;

Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTOCR 5
||:||
Db 21 YTRCR 25

RESULT 12

RS14_HELPJ STANDARD; PRT; 61 AA.

ID RS14_HELPJ STANDARD; PRT; 61 AA.

AC 092055; RA

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 30S ribosomal protein S14.

GN RPSN OR JHP1226.

OS Helicobacter pylori (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.

RN NCBI_TaxID=85963;
RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=26695 / ATCC 700392;

RC MEDLINE=97394467; PubMed=9252185;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirtness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gooley J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;

RT "The complete genome sequence of the gastric pathogen Helicobacter pylori." Nature 388:539-547(1997).

RL Nature 388:539-547(1997).

CC -!- FUNCTION: KNOWN TO BE REQUIRED FOR THE ASSEMBLY OF 30S PARTICLES AND MAY ALSO BE RESPONSIBLE FOR DETERMINING THE CONFORMATION OF THE 16S RNA (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

DR EMBL: AE000633; AAC083611; .

DR TIGR: HP1306; .

DR InterPro: IPR001209; Ribosomal_S14.

DR Pfam: PF00253; Ribosomal_S14; 1.

DR PROSITE: PS00527; RIBOSOMAL_S14; 1.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 61 AA; 7042 MW; EB4D764FCF507AB6 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 61;
Best local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTOCR 5
||:||
Db 21 YTRCR 25

RESULT 13

RS14_HELPY STANDARD; PRT; 61 AA.

ID RS14_HELPY STANDARD; PRT; 89 AA.

AC 042328; RA

DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Putative trypsin inhibitor ATT1-2 precursor.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Arabidopsis; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ccv. Columbia;

RA Harve C., Tremouaygue D., Lescure B.;

RT "Nucleotide sequence of an Arabidopsis cDNA encoding a serine protease inhibitor ATT1-2."

RL (Inv) Plant Gene Register PGR95-011.
RN [2]
RP CONCEPTUAL TRANSLATION.

RA Barroch A.;

RL Unpublished observations (JUN-1998).

CC -!- SIMILARITY: BELONGS TO THE ATT1-ATT1-2 PROTEASE INHIBITORS FAMILY.

CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; FRAMESHIFTS WERE

CC CORRECTED IN THE SIGNAL PEPTIDE REGION.

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or send an email to license@isb-sib.ch).

CC EMBL; Z46816; CAB68494; ALT_FRAME.
DR Interpro; IPR003614; Knot1.
SMART; SM0505; Knot1.
KW Serine protease inhibitor; signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 84 .PUTATIVE TRYPSIN INHIBITOR ATTI-2.
FT DISULFID 32 84 BY SIMILARITY.
FT DISULFID 45 69 BY SIMILARITY.
FT DISULFID 54 79 BY SIMILARITY.
FT DISULFID 58 81 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 89 AA: 991 MW: 35ECFD89E944E099 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Ov 1 YTCR 5
|||
Db 55 YTCR 59

Query Match 87.1%; Score 27; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Ov 1 YTCR 5
|||
Db 55 YTCR 59

Search completed: July 9, 2003, 12:00:45

Job time : 8.75 secs

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CC EMBL; AJ24958; CAB65481; -.
DR EMBL; AC002335; AAB643251; -.
DR Interpro; IPR003614; Knot1.
SMART; SM0505; Knot1.
KW Serine protease inhibitor; signal; Multigene family.
FT CHAIN 28 89 .PUTATIVE TRYPSIN INHIBITOR AT2G43510.
FT DISULFID 32 84 BY SIMILARITY.
FT DISULFID 45 69 BY SIMILARITY.
FT DISULFID 54 79 BY SIMILARITY.
FT DISULFID 58 81 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 89 AA: 9885 MW: C4FASD0B3ABB03DS CRC64;

Query Match 87.1%; Score 27; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Ov 1 YTCR 5
|||
Db 55 YTCR 59

RESULT 15
ITI3_ARATH STANDARD; PRT; 89 AA.
ID ITI3_ARATH
AC 022865;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative trypsin inhibitor At2g43510 precursor (didi 4T-1).
GN AT2G43510 OR T01024_25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
OC eudicots; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Talton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venczer J.C.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana." Nature 402:761-768(1999).
RL -1- SIMILARITY: BELONGS TO THE RTI/MTI-2 PROTEASE INHIBITORS FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use by non profit institutions as long as its content is in no way
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OM protein - protein search, using SW model

Run on: July 9, 2003, 11:57:21 ; Search time 17.75 Seconds

(without alignments), 58.041 Million cell updates/sec

Title: US-09-051-058-3
Perfect score: 31
Sequence: 1 YTQCR 5

Scoring table: BLOSUM52

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : SPTRIMBL_21; *

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query	Length	DB	ID	Description	RESULT ID	PRR130	PRR130	PRR130; PRELIMINARY;	PRR;	153 AA.
1	31	100.0	153	11	Q9R130								
2	31	100.0	153	11	Q9JK17	Q9R130 rattus norv							
3	31	100.0	155	11	Q9R134	Q9JK17 mus sexicol							
4	31	100.0	155	11	Q9R132	Q9JK17 rattus norv							
5	31	100.0	155	11	Q9R131	Q9R131 rattus norv							
6	31	100.0	155	11	Q9R127	Q9R131 rattus norv							
7	31	100.0	155	11	Q9R125	Q9R125 rattus norv							
8	31	100.0	155	11	Q9JK16	Q9R125 mus musculu							
9	31	100.0	155	11	Q9JK14	Q9R125 mus sexicol							
10	31	100.0	155	11	Q9JK12	Q9R125 mus sexicol							
11	31	100.0	155	11	Q9JK10	Q9R125 mus sexicol							
12	31	100.0	155	11	Q9JK9	Q9R125 mus sexicol							
13	31	100.0	155	11	Q9JK8	Q9R125 mus sexicol							
14	31	100.0	155	11	Q9JK3	Q9R125 mus sexicol							
15	31	100.0	155	11	Q9JK3	Q9R125 mus sexicol							
16	100.0	155	11	Q9R126	Q9R126 mus musculu								
17	31	100.0	155	11	Q9R127	Q9R126 mus musculu							
18	31	100.0	156	11	Q9R124	Q9R126 mus musculu							
19	31	100.0	156	11	Q9JKH7	Q9R126 mus caroli							
20	31	100.0	156	11	Q9JKH5	Q9R126 mus caroli							
21	31	100.0	156	11	Q9JKH4	Q9R126 mus caroli							
22	31	100.0	156	11	Q9JKH2	Q9R126 mus caroli							
23	31	100.0	156	11	Q9JKH1	Q9R126 mus caroli							
24	31	100.0	156	11	Q9JKH0	Q9R126 mus caroli							
25	31	100.0	156	11	Q9JKG9	Q9R126 mus caroli							
26	31	100.0	156	11	Q9JKG7	Q9R126 mus caroli							
27	31	100.0	156	11	Q9JKG6	Q9R126 mus caroli							
28	31	100.0	156	11	Q9JKF6	Q9R126 mus caroli							
29	31	100.0	156	11	Q9JKQ7	Q9R126 mus caroli							
30	31	100.0	156	11	Q9VHS0	Q9R126 mus caroli							
31	31	100.0	157	11	Q9JKJ8	Q9R126 mus caroli							
32	31	100.0	157	11	Q9JKJ7	Q9R126 mus caroli							
33	31	100.0	157	10	Q9SSV1	Q9R126 mus caroli							
34	31	100.0	155	11	Q9HE17	Q9R126 mus caroli							
35	28	90.3	148	2	Q9TW97	Q9R126 mus caroli							
36	28	90.3	148	2	Q9P961	Q9R126 rhizobium p							
37	28	90.3	151	5	Q9BHC6	Q9R126 rhizobium p							
38	28	90.3	267	12	Q9J4G9	Q9R126 salmonella							
39	28	90.3	304	16	Q9ZP52	Q9R126 salmonella							
40	41	90.3	307	2	Q93AP4	Q9R126 salmonella							
41	28	90.3	336	16	Q9PP25	Q9R126 campylobact							
42	28	90.3	394	3	Q9HE2	Q9R126 neurospora							
43	28	90.3	423	10	Q9fGR8	Q9R126 arabidopsis							
44	28	90.3	441	5	Q9W51	Q9R126 drosophila							
45	28	90.3	494	3	Q8X014	Q9R126 neurospora							

ALIGMENTS

RESULT 1	Q9R130	PRR130	PRR130; PRELIMINARY;	PRR;	153 AA.
	Q9R130;				
	AC				
	DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
	DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
	DR	Ribonuclease 7 precursor (Fragment).			
	GN	R7 .			
	OS	Rattus norvegicus (Rat).			
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
	NCBI_TaxID	10116;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE=20063179; PubMed=10594173;			
	RA	Sinchnaria N.A., Dyer K.D., Zhang J., Deering M.S., Bonville C.A., Domachowske J.B., Rosenberg H.F.;			
	RA	"Rapid evolution of the ribonuclease A superfamily: adaptive expansion of independent gene clusters in rats and mice."			
	RL	J. Mol. Evol. 49:721-728(1999).			
	DR	EMBL; AF171645; AAC51665.1; -.			
	HSSP	P00656; 2RNS.			
	DR	Intertpro; IPR001427; RNaseA.			
	DR	Pfam; PF00074; RNaseA; 1.			
	DR	PRINTS; PR0074; RIBONUCLEASE.			
	DR	PRODOM; P000535; RNaseA; 1.			
	DR	SMART; SM00092; RNase_Pc; 1.			
	DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
	KW	Signal.			
	FT	CHAIN 1 25 POTENTIAL.			
	FT	NON_TER 153 153 RIBONUCLEASE 7.			
	SQ	SEQUENCE 153 AA; 17679 MW; B5078251BA734D6B CRC64;			

Query Match 100.0%; Score 31; DB 11; Length 153;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 YTOCR 5
ID	Q9JKI7
AC	Q9JKI7;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Bostrophil-associated ribonuclease 4.
GN	EA4.
OS	MUS SAXICOLA (Spiny mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20243759; PubMed=10758160;
RA	Zhang J., Dyer K.D., Rosenberg H.F.;
RT	"Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";
RL	Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR	EMBL: AF238596; AAF67696.1; -.
DR	HSSP: P00655; 2RNS.
DR	InterPro: IPR01427; RNaseA.
DR	Pfam: PF00074; rnaseA_1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	PRODOM: PD000535; RNaseA_1.
DR	SMART: S00092; RNase_pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
SQ	SEQUENCE 153 AA; 17042 MN; CFF9982F0A6F296 CRC64;
QY	1 YTOCR 5
DB	115 YTOCR 119
RESULT 3	
ID	O9R134
AC	O9R134
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DR	01-MAY-2001 (TREMBLrel. 19, Last annotation update)
DR	Ribonuclease 4 precursor (Fragment).
GN	R4.
OS	Rattus norvegicus (Rat).
RA	Singhania N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A., Domachowske J.B., Rosenberg H.F.;
RT	"Rapid evolution of the ribonuclease A superfamily: adaptive expansion of independent gene clusters in rats and mice.";
RL	J. Mol. Biol. 49:721-726(1999).
DR	EMBL: AF171643; AAC51663.1; -.
DR	HSSP: P00656; 1RBD.
DR	InterPro: IPR01427; RNaseA.
DR	Pfam: PF00074; rnaseA_1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	PRODOM: PD000535; RNaseA_1.
DR	SMART: S00092; RNase_pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
ID	O9R132
AC	O9R132;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Ribonuclease 4 precursor (Fragment).
GN	R4.
OS	Rattus norvegicus (Rat).
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RT	"Rapid evolution of the ribonuclease A superfamily: adaptive expansion of independent gene clusters in rats and mice.";
RL	J. Mol. Biol. 49:721-726(1999).
DR	EMBL: AF171643; AAC51663.1; -.
DR	HSSP: P00656; 1RBD.
DR	InterPro: IPR01427; RNaseA.
DR	Pfam: PF00074; rnaseA_1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	PRODOM: PD000535; RNaseA_1.
DR	SMART: S00092; RNase_pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
ID	O9R131
AC	O9R131;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Ribonuclease 5 precursor (Fragment).
GN	R5.
OS	Rattus norvegicus (Rat).
RA	Singhania N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A., Domachowske J.B., Rosenberg H.F.;
RT	"Rapid evolution of the ribonuclease A superfamily: adaptive expansion of independent gene clusters in rats and mice.";
RL	J. Mol. Evol. 49:721-728(1999).
DR	EMBL: AF171641; AAC51661.1; -.
DR	HSSP: P00655; 2RNS.
DR	InterPro: IPR01427; RNaseA.
DR	Pfam: PF00074; rnaseA_1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	PRODOM: PD000535; RNaseA_1.
DR	SMART: S00092; RNase_pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.

RP
SEQUENCE FROM N.A.
RX
MEDLINE=20063779; PubMed=10594173;
RA
Sinchania N.A.; Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA
Domachowske J.B., Rosenberg H.F.; "Rapid evolution of the ribonuclease A superfamily: adaptive expansion
RT
of independent gene clusters in rats and mice.";
RL
J. Mol. Evol. 49:721-728(1999).
DR
EMBL: AF171644; AAD51664.1; -.
DR
HSSP: P00656; IRB.
DR
InterPro: IPR0147; RNaseA.
DR
Pfam: PF00074; rnaseA; I.
DR
PRINTS: PR0074; RIBONUCLEASE.
DR
ProDom: PD000535; RNaseA; 1.
DR
SMART: SM00092; RNase_Pc; 1.
DR
PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW
Signal.
FT
CHAIN 1 25 POTENTIAL.
FT
NON_TER 155 155 RIBONUCLEASE 5.
SQ
SEQUENCE 155 AA; 17189 MW; 35C6F3381DB92787 CRC64;
Query Match 100.0%; Score 31; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
1 YTOCR 5
Db
115 YTOCR 119

RESULT 6
Q9R127 PRELIMINARY; PRT; 155 AA.
ID Q9R127 AC
01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ribonuclease 14 precursor (fragment).
GN R14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TAXID=10116;
RN [1]
SEQUENCE FROM N.A.
RX
MEDLINE=20063779; PubMed=10594173;
RA
Sinchania N.A., Dyer K.D., Zhang J., Deming M.S., Bonville C.A.,
RA
Domachowske J.B., Rosenberg H.F.; "Rapid evolution of the ribonuclease A superfamily: adaptive expansion
RT
of independent gene clusters in rats and mice.";
RL
J. Mol. Evol. 49:721-728(1999).
DR
EMBL: AF171648; AAD51668.1; -.
DR
HSSP: P00656; IRB.
DR
InterPro: IPR001427; RNaseA.
DR
Pfam: PR00074; RNaseA; 1.
DR
PRINTS: PR00092; RNase_Pc; 1.
DR
ProDom: PD000535; RNaseA; 1.
DR
SMART: SM00092; RNase_Pc; 1.
DR
PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW
Signal.
FT
CHAIN 1 25 POTENTIAL.
FT
NON_TER 155 155 RIBONUCLEASE 8.
SQ
SEQUENCE 155 AA; 17364 MW; D594DB5129D6AE2B CRC64;
Query Match 100.0%; Score 31; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
1 YTOCR 5
Db
115 YTOCR 119

RESULT 8
09JK16 ID
09JK16 PRELIMINARY; PRT; 155 AA.
AC
09JK16; DT
01-OCT-2000 (TREMBLrel. 15, Created)
DT
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE
Biosinophil-associated ribonuclease 6.
GN
EAR6 OS
Mus saxicola (Spiny mouse).
OC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TAXID=10094;
RN [1]
SEQUENCE FROM N.A.
RX
MEDLINE=20043159; PubMed=10758160;
RA
Zhang J., Dyer K.D., Rosenberg H.F.;
RT
"Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL
Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR
EMBL: AF238397; AAC67697.1; -.
DR
HSSP: P00656; ILSQ.
DR
InterPro: IPR001427; RNaseA.
DR
Pfam: PR00074; RNaseA; 1.
DR
PRINTS: PR0074; RIBONUCLEASE.
DR
ProDom: PD000535; RNaseA; 1.
DR
SMART: SM00092; RNase_Pc; 1.

Query Match 100.0%; Score 31; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
1 YTOCR 5
Db
115 YTOCR 119

DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1;
 SQ SEQUENCE 155 AA; 17363 MW; BB5401FOC26CA1EF CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 115 YTQCR 119

RESULT 9

Q9JKI4 PRELIMINARY; PRT; 155 AA.

ID Q9JKI4; AC Q9JKI4; DT 01-OCT-2000 (TREMBrel. 15, Created)
 DE 01-JUN-2002 (TREMBrel. 21, Last annotation update)

Mus saxicola (Spiny mouse).
 Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=1094; [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2043759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene
 family by rapid gene sorting and positive selection.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000);
 DR EMBL; AF238399; AAF67699.1; -;
 DR InterPro; IPR01427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM0092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1;
 SQ SEQUENCE 155 AA; 17268 MW; D67163B6B0364A9 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 115 YTQCR 119

RESULT 10

Q9JKI2 PRELIMINARY; PRT; 155 AA.

ID Q9JKI2; AC Q9JKI2; DT 01-OCT-2000 (TREMBrel. 15, Created)
 DE 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE Eosinophil-associated ribonuclease 23.

OS Mus saxicola (Spiny mouse).
 OC Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=1094; [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2043759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene
 family by rapid gene sorting and positive selection.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000);
 DR EMBL; AF238401; AAF67701.1; -;
 DR HSSP; P00656; ILSQ.

DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1;
 SQ SEQUENCE 155 AA; 17367 MW; 5B4F44D97B0C5E25 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 115 YTQCR 119

RESULT 11

Q9JKI0 PRELIMINARY; PRT; 155 AA.

ID Q9JKI0; AC Q9JKI0; DT 01-OCT-2000 (TREMBrel. 15, Created)
 DE 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE Eosinophil-associated ribonuclease 7.

OS Mus phari (Shrew mouse).
 OC Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=1093; [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2043759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene
 family by rapid gene sorting and positive selection.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000);
 DR EMBL; AF238403; AAF67703.1; -;
 DR HSSP; P00656; ILSQ.
 DR InterPro; IPR01427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM0092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1;
 SQ SEQUENCE 155 AA; 17095 MW; 908C9F9A0C8498F CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTQCR 5
 Db 115 YTQCR 119

RESULT 12

Q9JKH9 PRELIMINARY; PRT; 155 AA.

ID Q9JKH9; AC Q9JKH9; DT 01-OCT-2000 (TREMBrel. 15, Created)
 DE 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE Eosinophil-associated ribonuclease 8.

OS Mus pahari (Shrew mouse).
 OC Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=1093; [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2043759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;

RT "Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";
 RT family; PRO. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000).
 RL SEQUENCE FROM N.A.
 RP
 DR EMBL: AF238404; AAF67704.1.; -.
 DR HSSP; P00556; JRNIS.
 DR InterPro: IPR001427; RNASEA.
 DR Pfam; PF00074; RNASE; 1.
 DR PRINTS; PRO0794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNASE; 1.
 DR SMART; SM00092; RNASE_P; 1.
 DR PROSITE; PS00121; RNASE_PANCREATIC; UNKNOWN_1.
 DR SEQUENCE 155 AA; 17385 MW; 965CB1185FD5809 CRC64;
 DR Pfam; PF00074; rnase; 1.
 DR PRINTS; PRO0794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNASE; 1.
 DR SMART; SM00092; RNASE_P; 1.
 DR PROSITE; PS00121; RNASE_PANCREATIC; UNKNOWN_1.
 DR SEQUENCE 155 AA; 17374 MW; BCEB17A83A553495 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHQCR 5
 Db 115 YHQCR 119

RESULT 13
 Q9JKHB
 ID Q9JKHB PRELIMINARY; PRT; 155 AA.
 AC Q9JKHB;
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Bosinophil-associated ribonuclease 12.
 GN EAR12.
 OS Mus caroli (Shrew mouse).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TAXID=10093;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20343755; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000).
 DR EMBL: AF238405; AAF67705.1; -.
 DR HSSP; P00556; 2RNS.
 DR InterPro: IPR001427; RNASE.
 DR Pfam: PF00074; rnase; 1.
 DR PRINTS; PRO0794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNASE; 1.
 DR SMART; SM00092; RNASE_P; 1.
 DR PROSITE; PS00121; RNASE_PANCREATIC; UNKNOWN_1.
 DR SEQUENCE 155 AA; 17167 MW; 651BB46C9F485A35 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHQCR 5
 Db 115 YHQCR 119

RESULT 14
 Q9JKH3
 ID Q9JKH3 PRELIMINARY; PRT; 155 AA.
 AC Q9JKH3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Bosinophil-associated ribonuclease 12.
 GN EAR12.
 OS Mus caroli (Wild mouse) (Ricefield mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TAXID=10089;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20343759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000).
 DR EMBL: AF238421; AAF67702.1; -.
 DR HSSP; P00556; 11SQ.
 DR InterPro: IPR001427; RNASE.
 DR Pfam: PF00074; rnase; 1.
 DR PRINTS; PRO0794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNASE; 1.
 DR SMART; SM00092; RNASE_P; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 DR SEQUENCE 155 AA; 17188 MW; A83B912B60CFDB39 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHQCR 5
 Db 115 YHQCR 119

OX NCBI_TAXID=10089;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL MEDLINE=20343759; PubMed=10758160;
 RA Zhang J., Dyer K.D., Rosenberg H.F.;
 RT "Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 97:4701-4706(2000).
 DR EMBL: AF238411; AAF67701.1; -.
 DR HSSP; P00656; 1LSQ.
 DR InterPro: IPR001427; RNASEA.
 DR Pfam; PF00074; rnase; 1.
 DR PRINTS; PRO0794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNASE; 1.
 DR SMART; SM00092; RNASE_P; 1.
 DR PROSITE; PS00121; RNASE_PANCREATIC; UNKNOWN_1.
 DR SEQUENCE 155 AA; 17374 MW; BCEB17A83A553495 CRC64;

Query Match 100.0%; Score 31; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHQCR 5
 Db 115 YHQCR 119

Search completed: July 9, 2003, 12:02:03
 Job time : 17.75 secs

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